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OM protein - protein search, using sw model

Run on: May 6, 2005, 17:11:07; Search time 16.8027 Seconds
(without alignments)
577.548 Million cell updates/sec

Title: US-10-072-159-11

Perfect score: 708
Sequence: 1 FSVGLETTYITPMPPIRFTK.....YADNNDSTFTGFLYHDTN 130

Scoring table:

BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

Issued Patents AA:
1: /cgn2_6/prodata/1/1aa/5A COMB.pep.*
2: /cgn2_6/prodata/1/1aa/5B COMB.pep.*
3: /cgn2_6/prodata/1/1aa/6A COMB.pep.*
4: /cgn2_6/prodata/1/1aa/6B COMB.pep.*
5: /cgn2_6/prodata/1/1aa/6C COMB.pep.*
6: /cgn2_6/prodata/1/1aa/6D COMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	708	100.0	130	3 US-09-485-316A-11	Sequence 11, App1
2	708	100.0	231	4 US-09-530-423-2	Sequence 2, App1
3	708	100.0	244	2 US-08-463-911-7	Sequence 7, App1
4	708	100.0	244	3 US-09-140-804-3	Sequence 3, App1
5	708	100.0	244	4 US-09-336-536-20	Sequence 20, App1
6	708	100.0	244	4 US-09-530-423-1	Sequence 1, App1
7	708	100.0	244	4 US-09-686-838B-3	Sequence 3, App1
8	708	100.0	244	4 US-09-911-176B-48	Sequence 48, App1
9	708	100.0	244	4 US-09-552-225A-3	Sequence 3, App1
10	708	100.0	244	4 US-09-619-740-51	Sequence 51, App1
11	708	100.0	244	4 US-09-776-976-6	Sequence 6, App1
12	708	100.0	244	4 US-09-909-547-6	Sequence 6, App1
13	708	100.0	244	4 US-09-569-852B-6	Sequence 6, App1
14	708	100.0	244	4 US-09-552-225A-3	Sequence 3, App1
15	655	92.5	130	3 US-09-485-316A-13	Sequence 13, App1
16	655	92.5	247	2 US-08-463-911-2	Sequence 2, App1
17	655	92.5	247	3 US-09-140-804-8	Sequence 8, App1
18	655	92.5	247	3 US-09-118-408-3	Sequence 3, App1
19	655	92.5	247	4 US-09-506-855-3	Sequence 8, App1
20	655	92.5	247	4 US-09-686-838B-8	Sequence 8, App1
21	655	92.5	247	4 US-09-911-176B-3	Sequence 3, App1
22	655	92.5	247	4 US-09-619-740-3	Sequence 3, App1
23	655	92.5	247	4 US-09-776-976-4	Sequence 4, App1
24	655	92.5	247	4 US-09-506-852-3	Sequence 3, App1
25	655	92.5	247	4 US-09-909-547-4	Sequence 4, App1
26	655	92.5	247	4 US-10-392-706-3	Sequence 3, App1
27	645	91.1	130	3 US-09-485-316A-12	Sequence 12, App1

28	645	91.1	247	4 US-09-776-976-2	Sequence 2, App1
29	645	91.1	247	4 US-09-909-547-2	Sequence 2, App1
30	287.5	40.6	680	4 US-09-949-001-15	Sequence 15, App1
31	287.5	40.6	680	4 US-09-949-001-20	Sequence 20, App1
32	280.5	39.6	161	3 US-09-415-551-3	Sequence 3, App1
33	280.5	39.6	161	3 US-09-975-607A-3	Sequence 3, App1
34	270.5	38.2	744	4 US-09-949-016-9607	Sequence 9607, App
35	266.5	37.6	285	4 US-09-312-283C-382	Sequence 382, App
36	266.5	37.6	284	3 US-09-188-930-295	Sequence 294, App
37	266.5	37.6	284	4 US-09-312-283C-294	Sequence 294, App
38	265.5	37.5	285	4 US-09-552-204A-2	Sequence 2, App
39	257.5	36.4	132	2 US-08-463-911-5	Sequence 5, App1
40	248.5	35.1	228	4 US-09-336-536-11	Sequence 11, App1
41	248.5	35.1	243	4 US-09-336-536-10	Sequence 10, App1
42	246.5	34.8	243	3 US-09-312-283C-295	Sequence 295, App
43	246.5	34.8	243	4 US-09-312-283C-295	Sequence 295, App
44	243.5	34.4	228	4 US-09-336-536-4	Sequence 4, App1
45	243.5	34.4	243	3 US-09-140-804-2	Sequence 2, App1

ALIGNMENTS

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RESULT 1
US-09-485-316A-11
; Sequence 11, Application US/09485316A
; Patent No. 6344441
; GENERAL INFORMATION:
; APPLICANT: Bihain, Bernard
; APPLICANT: Bouguerec, Lydie
; APPLICANT: Yen-Potin, Frances
; TITLE OF INVENTION: Lipoprotein-regulating medicaments
; FILE REFERENCE: GENSET.036APC
; CURRENT APPLICATION NUMBER: US/09/485,316A
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: FR 97/10088
; PRIOR FILING DATE: 1997-08-06
; PRIOR APPLICATION NUMBER: FR 98/05032
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: PCT IB98/01256
; PRIOR FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent.pm
; SEQ ID NO 11
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: 1..130
; OTHER INFORMATION: fragment 115..244 of translation from ref Genbank D45371
US-09-485-316A-11

Query Match      100.0%; Score 708; DB 3; Length 130;
Best Local Similarity 100.0%; Pred. No. 7.8e-80;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSVGLETTYITPMPPIRFTKIFPNQNNHYDSTGKHCNIPGLYYPAHYHTVMKQVKVS 60
Db 1 FSVGLETTYITPMPPIRFTKIFPNQNNHYDSTGKHCNIPGLYYPAHYHTVMKQVKVS 60
QY 61 LFKKDKAMLETTYDQYQENNVDQASGVLLHLEVDQDQVWLYQVGEGRNGLYADNNDSTP 120
Db 61 LFKKDKAMLETTYDQYQENNVDQASGVLLHLEVDQDQVWLYQVGEGRNGLYADNNDSTP 120
QY 121 TGFLLYHDTN 130
Db 121 TGFLLYHDTN 130

RESULT 2
US-09-530-423-2
; Sequence 2, Application US/09530423
```

Patent No. 6461821
GENERAL INFORMATION:
APPLICANT: Otsuka Pharmaceutical Co., Ltd.
TITLE OF INVENTION: Smooth muscle growth inhibitory composition, a
TITLE OF INVENTION: diagnostic method for arteriosclerosis and a kit
FILE REFERENCE: P98-51
CURRENT APPLICATION NUMBER: US/09/530,423
CURRENT FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: JP H9-297569
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 2
LENGTH: 231
TYPE: PRT
ORGANISM: Abdominal fat tissue from myoma uteri
US-09-530-423-2

Query Match 100.0%; Score 708; DB 4; Length 231;
Best Local Similarity 100.0%; Pred. No. 1.8e-79;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSVGLETVVTIPNMPIRFTKIFYNQNNHYDSTGKFCNIPGLYYFAHITVYMKDVYS 60
DB 102 FSVGLETVVTIPNMPIRFTKIFYNQNNHYDSTGKFCNIPGLYYFAHITVYMKDVYS 161

QY 61 LFKDKKMLFTYDYOENNVDAAGSVLLHLEVGQVWLQYVGGERNGLYADNDNSTF 120
DB 162 LFKDKKMLFTYDYOENNVDAAGSVLLHLEVGQVWLQYVGGERNGLYADNDNSTF 221

QY 121 TGFLLYHDTN 130
DB 222 TGFLLYHDTN 231

RESULT 3
US-08-463-911-7
Sequence 7, Application US/08463911
Patent No. 5869330
GENERAL INFORMATION:
APPLICANT: Scherer, Philipp E.
TITLE OF INVENTION: A NOVEL SERUM PROTEIN PRODUCED
TITLE OF INVENTION: EXCLUSIVELY IN ADIPOCYTES
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSER: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Millicta Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,911
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WH195-05
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 244 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-463-911-7

Query Match 100.0%; Score 708; DB 2; Length 244;
Best Local Similarity 100.0%; Pred. No. 1.9e-79;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSVGLETVVTIPNMPIRFTKIFYNQNNHYDSTGKFCNIPGLYYFAHITVYMKDVYS 60
DB 115 FSVGLETVVTIPNMPIRFTKIFYNQNNHYDSTGKFCNIPGLYYFAHITVYMKDVYS 174

QY 61 LFKDKKMLFTYDYOENNVDAAGSVLLHLEVGQVWLQYVGGERNGLYADNDNSTF 120
DB 175 LFKDKKMLFTYDYOENNVDAAGSVLLHLEVGQVWLQYVGGERNGLYADNDNSTF 234

QY 121 TGFLLYHDTN 130
DB 235 TGFLLYHDTN 244

RESULT 4
US-09-140-804-3
Sequence 3, Application US/09140804
Patent No. 6197930
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
FILE REFERENCE: 97-49
CURRENT APPLICATION NUMBER: US/09/140,804
CURRENT FILING DATE: 1998-08-26
EARLIER APPLICATION NUMBER: 60/056,983
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 3
LENGTH: 244
TYPE: PRT
ORGANISM: Homo sapiens
US-09-140-804-3

Query Match 100.0%; Score 708; DB 3; Length 244;
Best Local Similarity 100.0%; Pred. No. 1.9e-79;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSVGLETVVTIPNMPIRFTKIFYNQNNHYDSTGKFCNIPGLYYFAHITVYMKDVYS 60
DB 115 FSVGLETVVTIPNMPIRFTKIFYNQNNHYDSTGKFCNIPGLYYFAHITVYMKDVYS 174

QY 61 LFKDKKMLFTYDYOENNVDAAGSVLLHLEVGQVWLQYVGGERNGLYADNDNSTF 120
DB 175 LFKDKKMLFTYDYOENNVDAAGSVLLHLEVGQVWLQYVGGERNGLYADNDNSTF 234

QY 121 TGFLLYHDTN 130
DB 235 TGFLLYHDTN 244

RESULT 5
US-09-336-536-20
Sequence 20, Application US/09336536
Patent No. 6406884
GENERAL INFORMATION:
APPLICANT: Leiby, K.
APPLICANT: McKay, C.
APPLICANT: Bossone, S.
TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
FILE REFERENCE: 7853-144
CURRENT APPLICATION NUMBER: US/09/336,536
CURRENT FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patent In Ver. 2.0

SEQ ID NO 20
LENGTH: 244
TYPE: PRT
ORGANISM: Homo sapiens
US-09-336-536-20

Query Match
Best Local Similarity 100.0%; Score 708; DB 4; Length 244;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSVGLETTYVTIPMPPIRFTKIFPNQONHYDGSFGKHCNIPGLYYFAYHITVYMKDVKS 60
DB 115 FSVGLETTYVTIPMPPIRFTKIFPNQONHYDGSFGKHCNIPGLYYFAYHITVYMKDVKS 174
QY 61 LFKKDKAMLETTYDQYQENNVDAAGSVLHLLEVGDQVWLQVYGEGERNGLYADNDNSTF 120
DB 175 LFKKDKAMLETTYDQYQENNVDAAGSVLHLLEVGDQVWLQVYGEGERNGLYADNDNSTF 234
QY 121 TGFLLYHDTN 130
DB 235 TGFLLYHDTN 244

RESULT 6

US-09-530-423-1

Sequence 1, Application US/09530423

Patent No. 6461821

GENERAL INFORMATION:

APPLICANT: Otsuka Pharmaceutical Co., Ltd.

TITLE OF INVENTION: Smooth muscle growth inhibitory composition, a

TITLE OF INVENTION: diagnostic method for arteriosclerosis and a kit

FILE REFERENCE: P98-51

CURRENT APPLICATION NUMBER: US/09/530.423

CURRENT FILING DATE: 2000-05-01

PRIOR APPLICATION NUMBER: JP H9-297569

PRIOR FILING DATE: 1997-10-29

NUMBER OF SEQ ID NOS: 4

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1

LENGTH: 244

TYPE: PRT

ORGANISM: Abdominal fat tissue from myoma uteri

US-09-530-423-1

Query Match
Best Local Similarity 100.0%; Score 708; DB 4; Length 244;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSVGLETTYVTIPMPPIRFTKIFPNQONHYDGSFGKHCNIPGLYYFAYHITVYMKDVKS 60
DB 115 FSVGLETTYVTIPMPPIRFTKIFPNQONHYDGSFGKHCNIPGLYYFAYHITVYMKDVKS 174
QY 61 LFKKDKAMLETTYDQYQENNVDAAGSVLHLLEVGDQVWLQVYGEGERNGLYADNDNSTF 120
DB 175 LFKKDKAMLETTYDQYQENNVDAAGSVLHLLEVGDQVWLQVYGEGERNGLYADNDNSTF 234
QY 121 TGFLLYHDTN 130
DB 235 TGFLLYHDTN 244

RESULT 7

US-09-686-838B-3

Sequence 3, Application US/09686838B

Patent No. 6482612

GENERAL INFORMATION:

APPLICANT: Sheppard, Paul O.

TITLE OF INVENTION: Humes, Jacqueline M.

FILE REFERENCE: 97-49D1

CURRENT APPLICATION NUMBER: US/09/686.838B

CURRENT FILING DATE: 2000-10-10

PRIOR APPLICATION NUMBER: US 09/140,804
PRIOR FILING DATE: 1998-08-26
PRIOR APPLICATION NUMBER: US 60/056,983
PRIOR FILING DATE: 1997-08-26
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3

Query Match
Best Local Similarity 100.0%; Score 708; DB 4; Length 244;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSVGLETTYVTIPMPPIRFTKIFPNQONHYDGSFGKHCNIPGLYYFAYHITVYMKDVKS 60
DB 115 FSVGLETTYVTIPMPPIRFTKIFPNQONHYDGSFGKHCNIPGLYYFAYHITVYMKDVKS 174
QY 61 LFKKDKAMLETTYDQYQENNVDAAGSVLHLLEVGDQVWLQVYGEGERNGLYADNDNSTF 120
DB 175 LFKKDKAMLETTYDQYQENNVDAAGSVLHLLEVGDQVWLQVYGEGERNGLYADNDNSTF 234
QY 121 TGFLLYHDTN 130
DB 235 TGFLLYHDTN 244

RESULT 8

US-09-911-176B-48

Sequence 48, Application US/09911176B

Patent No. 6518403

GENERAL INFORMATION:

APPLICANT: Sheppard, Paul O.

TITLE OF INVENTION: ANTIBODIES THAT BIND AN

TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOG

FILE REFERENCE: 97-30D1

CURRENT APPLICATION NUMBER: US/09/911.176B

CURRENT FILING DATE: 2001-07-23

PRIOR APPLICATION NUMBER: 09/118,408

PRIOR FILING DATE: 1998-07-17

PRIOR APPLICATION NUMBER: 60/053,154

PRIOR FILING DATE: 1997-07-18

NUMBER OF SEQ ID NOS: 52

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 48

LENGTH: 244

TYPE: PRT

ORGANISM: Homo sapiens

US-09-911-176B-48

Query Match
Best Local Similarity 100.0%; Score 708; DB 4; Length 244;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSVGLETTYVTIPMPPIRFTKIFPNQONHYDGSFGKHCNIPGLYYFAYHITVYMKDVKS 60
DB 115 FSVGLETTYVTIPMPPIRFTKIFPNQONHYDGSFGKHCNIPGLYYFAYHITVYMKDVKS 174
QY 61 LFKKDKAMLETTYDQYQENNVDAAGSVLHLLEVGDQVWLQVYGEGERNGLYADNDNSTF 120
DB 175 LFKKDKAMLETTYDQYQENNVDAAGSVLHLLEVGDQVWLQVYGEGERNGLYADNDNSTF 234
QY 121 TGFLLYHDTN 130
DB 235 TGFLLYHDTN 244

RESULT 9

US-09-552-225A-3

Sequence 3, Application US/09552225A

Patent No. 6521233

US-09-552-225A-3
Sequence 3, Application US/09552225A
Patent No. 6521233

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; GENERAL INFORMATION:
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Bishop, Paul
; TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOG ZACBP3
; FILE REFERENCE: 99-09
; CURRENT APPLICATION NUMBER: US/09/552,225A
; CURRENT FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: 60/130,199
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 3
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-552-225A-3

Query Match          100.0%; Score 708; DB 4; Length 244;
Best Local Similarity 100.0%; Pred. No. 1.9e-79;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSVGLETVVITIPNMFIRFTKIFYNQONHYDSTGKFCNIPGLYFAVHITVYMKDVYS 60
    |||||||
Db 115 FSVGLETVVITIPNMFIRFTKIFYNQONHYDSTGKFCNIPGLYFAVHITVYMKDVYS 174

QY 61 LFKKDKAMLFTYDOYQENNVDAQSGSVLLHLEVGQVWLQYVGGERGGLYADNDNDSTF 120
    |||||||
Db 175 LFKKDKAMLFTYDOYQENNVDAQSGSVLLHLEVGQVWLQYVGGERGGLYADNDNDSTF 234

QY 121 TGFLLYHDTN 130
    |||||||
Db 235 TGFLLYHDTN 244

RESULT 10
US-09-619-740-51
; Sequence 51, Application US/09619740
; Patent No. 6544946
; GENERAL INFORMATION:
; APPLICANT: Shepard, Paul O.
; APPLICANT: Lasser, Gerald W.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: INHIBITORS FOR USE IN HEMOSTASIS AND IMMUNE FUNCTION
; FILE REFERENCE: 99-12C3
; CURRENT APPLICATION NUMBER: US/09/619,740
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/253,604
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/444,794
; PRIOR FILING DATE: 1999-11-22
; PRIOR APPLICATION NUMBER: 09/506,855
; PRIOR FILING DATE: 2000-02-17
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 51
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-619-740-51

Query Match          100.0%; Score 708; DB 4; Length 244;
Best Local Similarity 100.0%; Pred. No. 1.9e-79;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSVGLETVVITIPNMFIRFTKIFYNQONHYDSTGKFCNIPGLYFAVHITVYMKDVYS 60
    |||||||
Db 115 FSVGLETVVITIPNMFIRFTKIFYNQONHYDSTGKFCNIPGLYFAVHITVYMKDVYS 174

QY 61 LFKKDKAMLFTYDOYQENNVDAQSGSVLLHLEVGQVWLQYVGGERGGLYADNDNDSTF 120
    |||||||
Db 175 LFKKDKAMLFTYDOYQENNVDAQSGSVLLHLEVGQVWLQYVGGERGGLYADNDNDSTF 234

QY 121 TGFLLYHDTN 130
    |||||||
Db 235 TGFLLYHDTN 244
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Db 235 TGFLLYHDTN 244
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RESULT 11
US-09-776-976-6
; Sequence 6, Application US/09776976
; Patent No. 6566332
; GENERAL INFORMATION:
; APPLICANT: Fruebis, Joachim
; APPLICANT: Erickson, Mary Ruth
; APPLICANT: Yen, Frances
; APPLICANT: Bihain, Bernard
; TITLE OF INVENTION: OBG3 Globular Head and Uses Thereof for Decreasing Body Mass
; FILE REFERENCE: 76-US4,REG
; CURRENT APPLICATION NUMBER: US/09/776,976
; CURRENT FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/758,055
; PRIOR FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: US 60/176,228
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: US 60/198,087
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: US 60/299,881
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent.pm
; SEQ ID NO 6
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-776-976-6

Query Match          100.0%; Score 708; DB 4; Length 244;
Best Local Similarity 100.0%; Pred. No. 1.9e-79;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSVGLETVVITIPNMFIRFTKIFYNQONHYDSTGKFCNIPGLYFAVHITVYMKDVYS 60
    |||||||
Db 115 FSVGLETVVITIPNMFIRFTKIFYNQONHYDSTGKFCNIPGLYFAVHITVYMKDVYS 174

QY 61 LFKKDKAMLFTYDOYQENNVDAQSGSVLLHLEVGQVWLQYVGGERGGLYADNDNDSTF 120
    |||||||
Db 175 LFKKDKAMLFTYDOYQENNVDAQSGSVLLHLEVGQVWLQYVGGERGGLYADNDNDSTF 234

QY 121 TGFLLYHDTN 130
    |||||||
Db 235 TGFLLYHDTN 244

RESULT 12
US-09-909-547-6
; Sequence 6, Application US/09909547
; Patent No. 6579852
; GENERAL INFORMATION:
; APPLICANT: Fruebis, Joachim
; APPLICANT: Erickson, Mary Ruth
; APPLICANT: Yen, Frances
; APPLICANT: Bihain, Bernard
; TITLE OF INVENTION: OBG3 Globular Head and Uses Thereof for Decreasing Body Mass
; FILE REFERENCE: 76-US6,CIP
; CURRENT APPLICATION NUMBER: US/09/909,547
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 09/776,976
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/758,055
; PRIOR FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: US 60/299,881
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: US 60/198,087
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: US 60/176,228
; PRIOR FILING DATE: 2000-01-14
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NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patent.pm
SEQ ID NO 6
LENGTH: 244
TYPE: PRT
ORGANISM: Homo sapiens
US-09-909-547-6

Query Match 100.0%; Score 708; DB 4; Length 244;
Best Local Similarity 100.0%; Pred. No. 1.9e-79;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSVGLETTYITPMPPIRFTKIFYNQONHYDSTGKFKHCNIPGLYFAVHITVYMKDVKS 60
115 FSVGLETTYITPMPPIRFTKIFYNQONHYDSTGKFKHCNIPGLYFAVHITVYMKDVKS 174
QY 61 LFKKDKAMLFYDQYQENNVDQASGSVLLHLEVGDDQVWLQVYGEGRNGLYADNDNSTF 120
DB 175 LFKKDKAMLFYDQYQENNVDQASGSVLLHLEVGDDQVWLQVYGEGRNGLYADNDNSTF 234
QY 121 TGFLLYHDTN 130
DB 235 TGFLLYHDTN 244

RESULT 13

US-09-569-852B-6
Sequence 6, Application US/09569852B
Patent No. 6582909
GENERAL INFORMATION:
APPLICANT: Bougueleret, Lydie
APPLICANT: Bihain, Bernard
APPLICANT: Denison, Blake
APPLICANT: Yen-Potin, Frances
TITLE OF INVENTION: APM1 Biallelic Markers and Uses Thereof
FILE REFERENCE: GEN-113XC2
CURRENT APPLICATION NUMBER: US/09/569,852B
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: PCT/IB99/01858
PRIOR FILING DATE: 1999-11-04
PRIOR APPLICATION NUMBER: US 09/434,848
PRIOR FILING DATE: 1999-11-04
PRIOR APPLICATION NUMBER: US 60/119,593
PRIOR FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: US 60/107,113
PRIOR FILING DATE: 1998-11-04
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.1
SEQ ID NO 6
LENGTH: 244
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (15)..(15)
OTHER INFORMATION: The 'Xaa' at location 15 stands for Gly.
NAME/KEY: misc feature
LOCATION: (1)..(367)
OTHER INFORMATION: homology with 5' EST A254990 in private bank : GENSET
NAME/KEY: misc feature
LOCATION: (91)..(93)
OTHER INFORMATION: Amino acid at position 15 (Xaa) means Gly
NAME/KEY: misc feature
LOCATION: (15)..(15)
OTHER INFORMATION: The 'Xaa' at location 15 stands for Gly.
US-09-569-852B-6

Query Match 100.0%; Score 708; DB 4; Length 244;
Best Local Similarity 100.0%; Pred. No. 1.9e-79;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSVGLETTYITPMPPIRFTKIFYNQONHYDSTGKFKHCNIPGLYFAVHITVYMKDVKS 60
115 FSVGLETTYITPMPPIRFTKIFYNQONHYDSTGKFKHCNIPGLYFAVHITVYMKDVKS 174

DB 115 FSVGLETTYITPMPPIRFTKIFYNQONHYDSTGKFKHCNIPGLYFAVHITVYMKDVKS 174

QY 61 LFKKDKAMLFYDQYQENNVDQASGSVLLHLEVGDDQVWLQVYGEGRNGLYADNDNSTF 120

DB 175 LFKKDKAMLFYDQYQENNVDQASGSVLLHLEVGDDQVWLQVYGEGRNGLYADNDNSTF 234

QY 121 TGFLLYHDTN 130
DB 235 TGFLLYHDTN 244

RESULT 14

US-09-552-204A-3
Sequence 3, Application US/09552204A
Patent No. 6620909
GENERAL INFORMATION:
APPLICANT: Piddington, Christopher S.
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOG ZACRP2
FILE REFERENCE: 99-08
CURRENT APPLICATION NUMBER: US/09/552,204A
CURRENT FILING DATE: 2000-04-19
PRIOR APPLICATION NUMBER: 60/130,207
PRIOR FILING DATE: 1999-04-20
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 3
LENGTH: 244
TYPE: PRT
ORGANISM: Homo sapiens
US-09-552-204A-3

Query Match 100.0%; Score 708; DB 4; Length 244;
Best Local Similarity 100.0%; Pred. No. 1.9e-79;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSVGLETTYITPMPPIRFTKIFYNQONHYDSTGKFKHCNIPGLYFAVHITVYMKDVKS 60
115 FSVGLETTYITPMPPIRFTKIFYNQONHYDSTGKFKHCNIPGLYFAVHITVYMKDVKS 174
QY 61 LFKKDKAMLFYDQYQENNVDQASGSVLLHLEVGDDQVWLQVYGEGRNGLYADNDNSTF 120
DB 175 LFKKDKAMLFYDQYQENNVDQASGSVLLHLEVGDDQVWLQVYGEGRNGLYADNDNSTF 234
QY 121 TGFLLYHDTN 130
DB 235 TGFLLYHDTN 244

RESULT 15

US-09-485-316A-13
Sequence 13, Application US/09485316A
Patent No. 6344441
GENERAL INFORMATION:
APPLICANT: Bougueleret, Lydie
APPLICANT: Bihain, Bernard
APPLICANT: Yen-Potin, Frances
TITLE OF INVENTION: Lipoprotein-regulating medicaments
FILE REFERENCE: GENSET.036APC
CURRENT APPLICATION NUMBER: US/09/485,316A
CURRENT FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: FR 97/10088
PRIOR FILING DATE: 1997-08-06
PRIOR APPLICATION NUMBER: FR 98/05032
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: PCT IB98/01256
PRIOR FILING DATE: 1998-08-06
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patent.pm
SEQ ID NO 13
LENGTH: 130
TYPE: PRT
ORGANISM: Mus musculus

```

FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: 1..130
; OTHER INFORMATION: fragment 118..267 of translation from ref genbank U37222
US-09-485-316A-13

```

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Query Match          92.5%; Score 655; DB 3; Length 130;
Best Local Similarity 91.5%; Pred. No. 2.9e-73;
Matches 119; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

```

```

QY      1 FSVGLETVYVITIPNMPDIRFTKIFYNQONHYDSTGKFGHCNIPGLYYFAYHITVYMKDVKVS 60
Db      1 FSVGLETVYVITIPNMPDIRFTKIFYNQONHYDSTGKFGHCNIPGLYYFAYHITVYMKDVKVS 60
QY      61 LFKKDKAMLFYTDYQENNVDOAGSSVLLHLEVGDPQWLOVYGGGERNGLYADNDNDSTF 120
Db      61 LFKKDKAVLFTYDQYQENNVDOAGSSVLLHLEVGDPQWLOVYGGGERNGLYADNDNDSTF 120
QY      121 TGFLLYHDTN 130
Db      121 TGFLLYHDTN 130

```

Search completed: May 6, 2005, 17:33:03
 Job time : 17.8027 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 6, 2005, 17:05:01 / Search time 77.0651 Seconds
(without alignments)
652.420 Million cell updates/sec

Title: US-10-072-159-11

Perfect score: 708
Sequence: 1 FSVGLETYVTIPNMPIRFTK.....YADNNDSPFTGFLVHDTN 130

Scoring table:

BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	708	100.0	130	2	AAV01485
2	708	100.0	130	7	ADBS3609
3	708	100.0	137	7	ADBS3608
4	708	100.0	144	7	ADBS3607
5	708	100.0	145	7	ADBS3613
6	708	100.0	157	7	ADBS3606
7	708	100.0	163	7	ADBS3612
8	708	100.0	163	7	ADBS3655
9	708	100.0	187	7	ADBS3615
10	708	100.0	193	7	ADBS3614
11	708	100.0	203	7	ADBS3605
12	708	100.0	226	7	ADBS3604
13	708	100.0	231	7	AAV21808
14	708	100.0	231	4	AAAB0347
15	708	100.0	233	4	ADBS3530
16	708	100.0	244	2	ADBS3530
17	708	100.0	244	3	AAV21807
18	708	100.0	244	3	AAV71053
19	708	100.0	244	3	AAAB30233
20	708	100.0	244	4	AAAB5828
21	708	100.0	244	4	AAAB05528
22	708	100.0	244	4	AAAB49558
23	708	100.0	244	4	AAAB50373
24	708	100.0	244	4	AAAB49592
25	708	100.0	244	5	ABAB08223

ALIGNMENTS

RESULT 1	AAV01485	standard; peptide; 130 AA.
ID	AAV01485;	
AC	AAV01485;	
XX		
DT	21-MAY-1999	(first entry)
DE	ApM1 protein fragment (residues 115-244).	
XX		
XX	Dietary lipid; liver; peripheral tissue; medicament; C1q complement;	
KW	partitioning; lipolysis stimulated receptor; LSR; hypertension; G1q.R;	
KW	obesity; atherosclerosis; insulin resistance; obesity-related disease;	
KW	micronutrient; Type II diabetes; ocular lesion; renal lesion; cachexia;	
KW	neoplastic; eating disorder; ApM1.	
OS	Homo sapiens.	
XX		
PN	WO9907736-A2.	
XX		
PD	18-FEB-1999.	
XX		
PF	06-AUG-1998;	98WO-IB001256.
XX		
PR	06-AUG-1997;	97FR-00010088.
PR	22-APR-1998;	98FR-00005032.
XX		
PA	(GEST) GENSET.	
XX	(INRM) INSERM INST NAT SANTE & RECH MEDICALE.	
PI	Bihain B, Bouguetere L, Yen-Potin F,	
XX		
DR	WPI, 1999-167364/14.	
XX		
PT	Use of lipolysis stimulated receptor - for developing agents for	
PT	modulating partitioning of dietary lipids between the liver and	
PT	peripheral tissues, e.g. for treating obesity.	
XX		
PS	Claim 6, Page 70; 77pp; English.	
XX		
CC	The invention relates to agents which influence the partitioning of	
CC	dietary lipids between the liver and peripheral tissues for use as	
CC	medicaments. Sequences shown in AAV01481-488 that relate to C1q	
CC	complement family and two consensus sequences (AAV01499-500) are	
CC	particularly useful as such agents. Compounds that influence the	
CC	partitioning of dietary lipids between the liver and peripheral tissues	
CC	can be used in medicament for treating a condition in which the	
CC	partitioning of dietary lipids to the liver is abnormal. A polypeptide	

CC having binding specificity for a gamma subunit of the lipoplys
CC stimulated receptor (LSR) or a gcig.R or gcig.R homologue can be used for
CC treatment of obesity, where the polypeptide is not a subunit of the LSR.
CC The agents which increase partitioning of dietary lipids to the liver can
CC be used for treating obesity-related atherosclerosis, obesity-related
CC insulin resistance, obesity-related hypertension, microangiopathic lesions
CC resulting from obesity-related Type II diabetes, ocular lesions caused by
CC microangiopathy in obese individuals with Type II diabetes, and renal
CC lesions caused by microangiopathy in obese individuals with Type II
CC diabetes. Agents which decrease the partitioning of dietary lipids to the
CC liver can be used for treating cachexia in subjects with neoplastic or
CC para-neoplastic syndrome or eating disorders. The present sequence
CC represents a claimed peptide fragment of ApM1
XX

Sequence 130 AA;

Query Match 100.0%; Score 708; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 3.5e-78;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSVGLETVITIPNMPIRFTKIFYNQONHYDSTGKFKHCNIGLYFAVHITVYMKDVYS 60
DB 1 FSVGLETVITIPNMPIRFTKIFYNQONHYDSTGKFKHCNIGLYFAVHITVYMKDVYS 60
QY 61 LFKDKKAMLFYDYOENNVDQAGSVLLHLEVGQVWLQVYGEGERNGLYADNDNDSTF 120
DB 61 LFKDKKAMLFYDYOENNVDQAGSVLLHLEVGQVWLQVYGEGERNGLYADNDNDSTF 120

QY 121 TGFLLYHDTN 130
DB 121 TGFLLYHDTN 130

RESULT 2
ADE93609
ID ADE93609 standard; protein; 130 AA.

AC ADE93609;

DT 12-FEB-2004 (first entry)

DE Human adiponectin apM1(115-244) protein.

XX
KW adiponectin conjugate; antiarteriosclerotic; antidiabetic; cardiant;
KW antirheumatic; antibacterial; antilipemic; dermatological;
KW immunosuppressive; immunomodulator; anorectic; diabetes; obesity;
KW atherosclerosis; cardiovascular disease; dyslipidaemia;
KW rheumatoid arthritis; Crohn's; systemic lupus erythematosus;
KW Sjogren syndrome; cachexia; septic shock; myasthenia gravis;
KW myocardial infarction; inflammation; gene therapy; human; apM1;
KW wild-type.

XX Homo sapiens.

OS WO2003055916-A2.

PN 10-JUL-2003.

DE 20-DEC-2002; 2002WO-DK000897.

XX
PF 21-DEC-2001; 2001DK-00001952.
XX 21-DEC-2001; 2001US-0343482P.
XX 25-APR-2002; 2002DK-00000627.
XX 25-APR-2002; 2002US-0375492P.
XX 03-JUL-2002; 2002DK-00001036.
XX 03-JUL-2002; 2002US-0394117P.
XX 20-SEP-2002; 2002DK-00001385.
XX 20-SEP-2002; 2002US-0412169P.

PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.

XX Rasmussen PB, Andersen KV, Pedersen AH, Schambye HT, Halkier T;

PI Bogenes A;
XX
DR WPI; 2003-598262/56.

PT New conjugate comprising an adiponectin polypeptide and a first non-
PT polypeptide moiety, useful for preparing a composition for treating a
PT mammal having e.g., diabetes, atherosclerosis or cardiovascular disease.
XX
PS Claim 14; SEQ ID NO 7; 184pp; English.

XX The invention relates to a novel conjugate comprising an adiponectin
CC polypeptide and a first non-polypeptide moiety covalently attached to the
CC adiponectin polypeptide. The adiponectin polypeptide comprises an amino
CC residue having an attachment group for the first non-polypeptide
CC moiety which has been introduced in a position where the parent
CC adiponectin is occupied by a surface exposed amino acid residue. The
CC conjugate of the invention demonstrates antiarteriosclerotic,
CC antidiabetic, cardiant, antirheumatic, antibacterial, antilipemic,
CC dermatological, immunosuppressive, immunomodulator and anorectic
CC activities and may be useful for treating diabetes, obesity,
CC atherosclerosis, cardiovascular diseases, dyslipidaemia, rheumatoid
CC arthritis, Crohn's disease, systemic lupus erythematosus, Sjogren
CC syndrome, cachexia, septic shock, myasthenia gravis, myocardial
CC infarction and destructive processes related to activation of the
CC inflammatory system, as well as during gene therapy procedures. The
CC current sequence is that of the human adiponectin apM1 protein of the
CC invention.

Sequence 130 AA;

Query Match 100.0%; Score 708; DB 7; Length 130;
Best Local Similarity 100.0%; Pred. No. 3.5e-78;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSVGLETVITIPNMPIRFTKIFYNQONHYDSTGKFKHCNIGLYFAVHITVYMKDVYS 60
DB 1 FSVGLETVITIPNMPIRFTKIFYNQONHYDSTGKFKHCNIGLYFAVHITVYMKDVYS 60

QY 61 LFKDKKAMLFYDYOENNVDQAGSVLLHLEVGQVWLQVYGEGERNGLYADNDNDSTF 120
DB 61 LFKDKKAMLFYDYOENNVDQAGSVLLHLEVGQVWLQVYGEGERNGLYADNDNDSTF 120

QY 121 TGFLLYHDTN 130
DB 121 TGFLLYHDTN 130

RESULT 3
ADE93608
ID ADE93608 standard; protein; 137 AA.

AC ADE93608;

DT 12-FEB-2004 (first entry)

DE Human adiponectin apM1(108-244) protein.

XX
KW adiponectin conjugate; antiarteriosclerotic; antidiabetic; cardiant;
KW antirheumatic; antibacterial; antilipemic; dermatological;
KW immunosuppressive; immunomodulator; anorectic; diabetes; obesity;
KW atherosclerosis; cardiovascular disease; dyslipidaemia;
KW rheumatoid arthritis; Crohn's; systemic lupus erythematosus;
KW Sjogren syndrome; cachexia; septic shock; myasthenia gravis;
KW myocardial infarction; inflammation; gene therapy; human; apM1;
KW wild-type.

XX Homo sapiens.

OS WO2003055916-A2.

PN 10-JUL-2003.

DE 20-DEC-2002; 2002WO-DK000897.

```

XX 21-DEC-2001; 2001DK-00001952.
PR 21-DEC-2001; 2001US-0343482P.
PR 25-APR-2002; 2002DK-0000627.
PR 25-APR-2002; 2002US-0375492P.
PR 03-JUL-2002; 2002DK-00001036.
PR 03-JUL-2002; 2002US-0394117P.
PR 20-SEP-2002; 2002DK-00001385.
PR 20-SEP-2002; 2002US-0412169P.
XX
XX (MAXY-) MAXYGEN APS.
XX (MAXY-) MAXYGEN HOLDINGS LTD.
XX
XX Rasmussen PB, Andersen KV, Pedersen AH, Schambye HT, Halkier T;
XX Bogness A;
XX
XX WPI; 2003-598262/56;
XX
XX New conjugate comprising an adiponectin polypeptide and a first non-
XX polypeptide moiety, useful for preparing a composition for treating a
XX mammal having e.g., diabetes, atherosclerosis or cardiovascular disease.
XX
XX Claim 14; SEQ ID NO 6; 184pp; English.
XX
XX The invention relates to a novel conjugate comprising an adiponectin
XX polypeptide and a first non-polypeptide moiety covalently attached to the
XX adiponectin polypeptide. The adiponectin polypeptide comprises an amino
XX acid residue having an attachment group for the first non-polypeptide
XX moiety which has been introduced in a position where the parent
XX adiponectin is occupied by a surface exposed amino acid residue. The
XX conjugate of the invention demonstrates antiarteriosclerotic,
XX antidiabetic, cardiac, antirheumatic, antibacterial, antilipemic,
XX dermatological, immunosuppressive, immunomodulator and anorectic
XX activities and may be useful for treating diabetes, obesity,
XX atherosclerosis, cardiovascular diseases, dyslipidaemia, rheumatoid
XX arthritis, Crohn's disease, systemic lupus erythematosus, Sjogren
XX syndrome, cachexia, septic shock, myasthenia gravis, myocardial
XX infarction and destructive processes related to activation of the
XX inflammatory system, as well as during gene therapy procedures. The
XX current sequence is that of the human adiponectin apM1 protein of the
XX invention.
XX
XX Sequence 137 AA;
XX
XX Query Match 100.0%; Score 708; DB 7; Length 137;
XX Best Local Similarity 100.0%; Pred. No. 3,8e-78;
XX Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 FSVGLETTYTIPMPPIRFTKIFPNQONHYDGSFGKHCNIPGLYFAVYHITVYMKDVKS 60
XX 8 FSVGLETTYTIPMPPIRFTKIFPNQONHYDGSFGKHCNIPGLYFAVYHITVYMKDVKS 67
XX
XX 61 LFKKDKAMLFYTDQYOENNVDQASGSVLLHLEVGDDQVWLQVYGEGRNGLYADNDSTF 120
XX 68 LFKKDKAMLFYTDQYOENNVDQASGSVLLHLEVGDDQVWLQVYGEGRNGLYADNDSTF 127
XX
XX 121 TGFLLYHDTN 130
XX 128 TGFLLYHDTN 137
XX
XX RESULT 4
XX ADE93607 standard; protein; 144 AA.
XX
XX ADE93607;
XX
XX 12-FEB-2004 (first entry)
XX
XX Human adiponectin apM1 (101-244) protein.
XX
XX adiponectin conjugate; antiarteriosclerotic; antidiabetic; cardiac;
XX antirheumatic; antibacterial; antilipemic; dermatological;

```

```

KM immunosuppressive; immunomodulator; anorectic; diabetes; obesity;
KM atherosclerosis; cardiovascular disease; dyslipidaemia;
KM rheumatoid arthritis; Crohn's; systemic lupus erythematosus;
KM Sjogren syndrome; cachexia; septic shock; myasthenia gravis;
KM myocardial infarction; inflammation; gene therapy; human; apM1;
KM wild-type.
XX
XX Homo sapiens.
XX
XX WO2003055916-A2.
XX
XX 10-JUL-2003.
XX
XX 20-DEC-2002; 2002MO-DK000897.
XX
XX 21-DEC-2001; 2001DK-00001952.
XX 21-DEC-2001; 2001US-0343482P.
XX 25-APR-2002; 2002DK-0000627.
XX 25-APR-2002; 2002US-0375492P.
XX 03-JUL-2002; 2002DK-00001036.
XX 03-JUL-2002; 2002US-0394117P.
XX 20-SEP-2002; 2002DK-00001385.
XX 20-SEP-2002; 2002US-0412169P.
XX
XX (MAXY-) MAXYGEN APS.
XX (MAXY-) MAXYGEN HOLDINGS LTD.
XX
XX Rasmussen PB, Andersen KV, Pedersen AH, Schambye HT, Halkier T;
XX Bogness A;
XX
XX WPI; 2003-598262/56.
XX
XX New conjugate comprising an adiponectin polypeptide and a first non-
XX polypeptide moiety, useful for preparing a composition for treating a
XX mammal having e.g., diabetes, atherosclerosis or cardiovascular disease.
XX
XX Claim 44; SEQ ID NO 5; 184pp; English.
XX
XX The invention relates to a novel conjugate comprising an adiponectin
XX polypeptide and a first non-polypeptide moiety covalently attached to the
XX adiponectin polypeptide. The adiponectin polypeptide comprises an amino
XX acid residue having an attachment group for the first non-polypeptide
XX moiety which has been introduced in a position where the parent
XX adiponectin is occupied by a surface exposed amino acid residue. The
XX conjugate of the invention demonstrates antiarteriosclerotic,
XX antidiabetic, cardiac, antirheumatic, immunomodulator and anorectic
XX activities and may be useful for treating diabetes, obesity,
XX atherosclerosis, cardiovascular diseases, dyslipidaemia, rheumatoid
XX arthritis, Crohn's disease, systemic lupus erythematosus, Sjogren
XX syndrome, cachexia, septic shock, myasthenia gravis, myocardial
XX infarction and destructive processes related to activation of the
XX inflammatory system, as well as during gene therapy procedures. The
XX current sequence is that of the human adiponectin apM1 protein of the
XX invention.
XX
XX Sequence 144 AA;
XX
XX Query Match 100.0%; Score 708; DB 7; Length 144;
XX Best Local Similarity 100.0%; Pred. No. 4,1e-78;
XX Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 FSVGLETTYTIPMPPIRFTKIFPNQONHYDGSFGKHCNIPGLYFAVYHITVYMKDVKS 60
XX 15 FSVGLETTYTIPMPPIRFTKIFPNQONHYDGSFGKHCNIPGLYFAVYHITVYMKDVKS 74
XX
XX 61 LFKKDKAMLFYTDQYOENNVDQASGSVLLHLEVGDDQVWLQVYGEGRNGLYADNDSTF 120
XX 75 LFKKDKAMLFYTDQYOENNVDQASGSVLLHLEVGDDQVWLQVYGEGRNGLYADNDSTF 134
XX
XX 121 TGFLLYHDTN 130
XX 135 TGFLLYHDTN 144
XX
XX Db

```

RESULT 5
ADE93613
ID ADE93613 standard; protein; 145 AA.

AC ADE93613;

DT 12-FEB-2004 (first entry)

DE Human adiponectin apM1(100-244) protein.

XX adiponectin conjugate; antiarteriosclerotic; antidiabetic; cardiant;
XX antirheumatic; antibacterial; antilipemic; dermatological;
KW immunosuppressive; immunomodulator; anorectic; diabetes; obesity;
KW atherosclerosis; cardiovascular disease; dyslipidaemia;
KW rheumatoid arthritis; Crohn's; systemic lupus erythematosus;
KW Sjogren syndrome; cachexia; septic shock; myasthenia gravis;
KW myocardial infarction; inflammation; gene therapy; human; apM1;
KW wild-type.

XX Homo sapiens.

OS WO2003055916-A2.

XX 10-JUL-2003.

PF 20-DEC-2002; 2002WO-DK000897.

PR 21-DEC-2001; 2001DK-00001952.

PR 21-DEC-2001; 2001US-0343482P.

PR 25-APR-2002; 2002DK-00000627.

PR 25-APR-2002; 2002US-0375492P.

PR 03-JUL-2002; 2002DK-00001036.

PR 03-JUL-2002; 2002US-0394117P.

PR 20-SEP-2002; 2002DK-00001385.

PR 20-SEP-2002; 2002US-0412169P.

XX (MAXY-) MAXYGEN APS.

PA (MAXY-) MAXYGEN HOLDINGS LTD.

XX Rasmussen PB, Andersen KV, Pedersen AH, Schambye HT, Halkier T;
PI Bognes A;

DR WPI; 2003-598262/56.

PT New conjugate comprising an adiponectin polypeptide and a first non-
PT polypeptide moiety, useful for preparing a composition for treating a
PT mammal having e.g., diabetes, atherosclerosis or cardiovascular disease.

PS Claim 4; SEQ ID NO 11; 184pp; English.

XX The invention relates to a novel conjugate comprising an adiponectin
CC polypeptide and a first non-polypeptide moiety covalently attached to the
CC adiponectin polypeptide. The adiponectin polypeptide comprises an amino
CC acid residue having an attachment group for the first non-polypeptide
CC moiety which has been introduced in a position where the parent
CC adiponectin is occupied by a surface exposed amino acid residue. The
CC conjugate of the invention demonstrates antiarteriosclerotic,
CC antidiabetic, cardiant, antirheumatic, antibacterial, antilipemic,
CC dermatological, immunosuppressive, immunomodulator and anorectic
CC activities and may be useful for treating diabetes, obesity,
CC atherosclerosis, cardiovascular diseases, dyslipidaemia, rheumatoid
CC arthritis, Crohn's disease, systemic lupus erythematosus, Sjogren
CC syndrome, cachexia, septic shock, myasthenia gravis, myocardial
CC infarction and destructive processes related to activation of the
CC inflammatory system, as well as during gene therapy procedures. The
CC current sequence is that of the human adiponectin apM1 protein of the
CC invention.

XX Sequence 145 AA;

Query Match 100.0%; Score 708; DB 7; Length 145;

Best Local Similarity 100.0%; Pred. No. 4.1e-78;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FSVGLETTYVTIPNNPIRFTKTFYNOQNHQOSTGKFRHCNIPGLYFAHITVYMKDVVS 60

DB 16 FSVGLETTYVTIPNNPIRFTKTFYNOQNHQOSTGKFRHCNIPGLYFAHITVYMKDVVS 75

OY 61 LFKKDKAMLFYTDYQENNVDAAGSVLHLFVGDQVWLQYVGGERNGLYADNDNSTF 120

DB 76 LFKKDKAMLFYTDYQENNVDAAGSVLHLFVGDQVWLQYVGGERNGLYADNDNSTF 135

OY 121 TGFLLYHDTN 130

DB 136 TGFLLYHDTN 145

RESULT 6
ADE93606
ID ADE93606 standard; protein; 157 AA.

AC ADE93606;

DT 12-FEB-2004 (first entry)

DE Human adiponectin apM1(88-244) protein.

XX adiponectin conjugate; antiarteriosclerotic; antidiabetic; cardiant;
XX antirheumatic; antibacterial; antilipemic; dermatological;
KW immunosuppressive; immunomodulator; anorectic; diabetes; obesity;
KW atherosclerosis; cardiovascular disease; dyslipidaemia;
KW rheumatoid arthritis; Crohn's; systemic lupus erythematosus;
KW Sjogren syndrome; cachexia; septic shock; myasthenia gravis;
KW myocardial infarction; inflammation; gene therapy; human; apM1;
KW wild-type.

XX Homo sapiens.

OS WO2003055916-A2.

XX 10-JUL-2003.

PF 20-DEC-2002; 2002WO-DK000897.

PR 21-DEC-2001; 2001DK-00001952.

PR 21-DEC-2001; 2001US-0343482P.

PR 25-APR-2002; 2002DK-00000627.

PR 25-APR-2002; 2002US-0375492P.

PR 03-JUL-2002; 2002DK-00001036.

PR 03-JUL-2002; 2002US-0394117P.

PR 20-SEP-2002; 2002DK-00001385.

PR 20-SEP-2002; 2002US-0412169P.

XX (MAXY-) MAXYGEN APS.

PA (MAXY-) MAXYGEN HOLDINGS LTD.

XX Rasmussen PB, Andersen KV, Pedersen AH, Schambye HT, Halkier T;
PI Bognes A;

DR WPI; 2003-598262/56.

PT New conjugate comprising an adiponectin polypeptide and a first non-
PT polypeptide moiety, useful for preparing a composition for treating a
PT mammal having e.g., diabetes, atherosclerosis or cardiovascular disease.

PS Claim 4; SEQ ID NO 4; 184pp; English.

XX The invention relates to a novel conjugate comprising an adiponectin
CC polypeptide and a first non-polypeptide moiety covalently attached to the
CC adiponectin polypeptide. The adiponectin polypeptide comprises an amino
CC acid residue having an attachment group for the first non-polypeptide
CC moiety which has been introduced in a position where the parent
CC adiponectin is occupied by a surface exposed amino acid residue. The
CC conjugate of the invention demonstrates antiarteriosclerotic,

CC anti-diabetic, cardiant, anti-rheumatic, anti-bacterial, anti-lipemic,
CC dermatological, immunosuppressive, immunomodulator and anorectic
CC activities and may be useful for treating diabetes, obesity,
CC atherosclerosis, cardiovascular diseases, dyslipidaemia, rheumatoid
CC arthritis, Crohn's disease, systemic lupus erythematosus, Sjogren
CC syndrome, cachexia, septic shock, myasthenia gravis, myocardial
CC infarction and destructive processes related to activation of the
CC inflammatory system, as well as during gene therapy procedures. The
CC current sequence is that of the human adiponectin apM1 protein of the
CC invention.
XX
XX
SQ Sequence 157 AA;
Query Match 100.0%; Score 708; DB 7; Length 157;
Best Local Similarity 100.0%; Pred. No. 4, 6e-78;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FSVGLETTYITPMPRIPTKIFYNQONHYDGSIGKFKHCNIPGLYFAVHITVYMKDVKS 60
DB 28 FSVGLETTYITPMPRIPTKIFYNQONHYDGSIGKFKHCNIPGLYFAVHITVYMKDVKS 87
QY 61 LFKKDKAMLFYDQYQENNVDQSGSVLLHLEVGDDVWLQVYGEGERNGLYADNDNSTF 120
DB 88 LFKKDKAMLFYDQYQENNVDQSGSVLLHLEVGDDVWLQVYGEGERNGLYADNDNSTF 147
QY 121 TGFLLYHDTN 130
DB 148 TGFLLYHDTN 157
RESULT 7
ADE93612
ID ADE93612 standard; protein; 163 AA.
XX
XX ADE93612;
DT 12-FEB-2004 (first entry)
XX
DE Human adiponectin apM1 (82-244) protein.
XX
XX adiponectin conjugate; anti-arteriosclerotic; anti-diabetic; cardiant;
XX anti-rheumatic; anti-bacterial; anti-lipemic; dermatological;
XX immunosuppressive; immunomodulator; anorectic; diabetes; obesity;
XX atherosclerosis; cardiovascular diseases; dyslipidaemia;
XX rheumatoid arthritis; Crohn's; systemic lupus erythematosus;
XX Sjogren syndrome; cachexia; septic shock; myasthenia gravis;
XX myocardial infarction; inflammation; gene therapy; human; apM1;
XX wild-type.
XX
OS Homo sapiens.
XX
XX WO2003055916-A2.
XX
XX 10-JUL-2003.
XX
XX 20-DEC-2002; 2002WO-DK000897.
XX
XX 21-DEC-2001; 2001DK-00001952.
XX 21-DEC-2001; 2001US-0343482P.
XX 25-APR-2002; 2002DK-00000627.
XX 25-APR-2002; 2002US-0375492P.
XX 03-JUL-2002; 2002DK-00001036.
XX 03-JUL-2002; 2002US-0394117P.
XX 20-SEP-2002; 2002DK-00001385.
XX 20-SEP-2002; 2002US-0412169P.
XX
XX (MAXY-) MAXYGEN APS.
XX (MAXY-) MAXYGEN HOLDINGS LTD.
XX
XX Raasmussen PB, Andersen KV, Pedersen AH, Schambye HT, Halkier T,
XX Bogness A;
XX
XX WPI; 2003-598262/56.

DR N-PSDB; ADE93618.
XX
XX PT New conjugate comprising an adiponectin polypeptide and a first non-
XX polypeptide moiety, useful for preparing a composition for treating a
XX mammal having e.g., diabetes, atherosclerosis or cardiovascular disease.
XX
XX Claim 44; SEQ ID NO 10; 184pp; English.
XX
XX The invention relates to a novel conjugate comprising an adiponectin
XX polypeptide and a first non-polypeptide moiety covalently attached to the
XX adiponectin polypeptide. The adiponectin polypeptide comprises an amino
XX acid residue having an attachment group for the first non-polypeptide
XX moiety which has been introduced in a position where the parent
XX adiponectin is occupied by a surface exposed amino acid residue. The
XX conjugate of the invention demonstrates anti-arteriosclerotic, anti-
XX anti-diabetic, cardiant, anti-rheumatic, anti-bacterial, anti-lipemic,
XX dermatological, immunosuppressive, immunomodulator and anorectic
XX activities and may be useful for treating diabetes, obesity,
XX atherosclerosis, cardiovascular diseases, dyslipidaemia, rheumatoid
XX arthritis, Crohn's disease, systemic lupus erythematosus, Sjogren
XX syndrome, cachexia, septic shock, myasthenia gravis, myocardial
XX infarction and destructive processes related to activation of the
XX inflammatory system, as well as during gene therapy procedures. The
XX current sequence is that of the human adiponectin apM1 protein of the
XX invention.
XX
XX
SQ Sequence 163 AA;
Query Match 100.0%; Score 708; DB 7; Length 163;
Best Local Similarity 100.0%; Pred. No. 4, 8e-78;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FSVGLETTYITPMPRIPTKIFYNQONHYDGSIGKFKHCNIPGLYFAVHITVYMKDVKS 60
DB 34 FSVGLETTYITPMPRIPTKIFYNQONHYDGSIGKFKHCNIPGLYFAVHITVYMKDVKS 93
QY 61 LFKKDKAMLFYDQYQENNVDQSGSVLLHLEVGDDVWLQVYGEGERNGLYADNDNSTF 120
DB 94 LFKKDKAMLFYDQYQENNVDQSGSVLLHLEVGDDVWLQVYGEGERNGLYADNDNSTF 153
QY 121 TGFLLYHDTN 130
DB 154 TGFLLYHDTN 163
RESULT 8
ADE93655
ID ADE93655 standard; protein; 163 AA.
XX
XX ADE93655;
AC
XX
XX 12-FEB-2004 (first entry)
XX
XX Human adiponectin Y11N-apM1 (82-244) mutant protein.
XX
XX
XX adiponectin conjugate; anti-arteriosclerotic; anti-diabetic; cardiant;
XX anti-rheumatic; anti-bacterial; anti-lipemic; dermatological;
XX immunosuppressive; immunomodulator; anorectic; diabetes; obesity;
XX atherosclerosis; cardiovascular diseases; dyslipidaemia;
XX rheumatoid arthritis; Crohn's; systemic lupus erythematosus;
XX Sjogren syndrome; cachexia; septic shock; myasthenia gravis;
XX myocardial infarction; inflammation; gene therapy; human; apM1; mutant;
XX mutcin.
XX
XX Synthetic.
XX Homo sapiens.
XX
XX WO2003055916-A2.
XX
XX 10-JUL-2003.
XX
XX 20-DEC-2002; 2002WO-DK000897.
XX
XX

PR 21-DEC-2001; 2001DK-00001952.
PR 21-DEC-2001; 2001US-0343482P.
PR 25-APR-2002; 2002DK-0000627.
PR 25-APR-2002; 2002US-0375492P.
PR 03-JUL-2002; 2002DK-00001036.
PR 03-JUL-2002; 2002US-0394117P.
PR 20-SEP-2002; 2002DK-00001385.
PR 20-SEP-2002; 2002US-0412169P.
XX
XX
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
XX
XX
PI Rasmussen PB, Andersen KV, Pedersen AH, Schambye HT, Halkier T;
PI Bogenes A;
XX
XX
DR MPI: 2003-598262/56.
DR N-PSDB; ADE93667.
XX
XX
PT New conjugate comprising an adiponectin polypeptide and a first non-
PT polypeptide moiety, useful for preparing a composition for treating a
PT mammal having e.g., diabetes, atherosclerosis or cardiovascular disease.
XX
XX
PS Claim 38; SEQ ID NO 53; 184bp; English.
XX
XX
CC The invention relates to a novel conjugate comprising an adiponectin
CC polypeptide and a first non-polypeptide moiety covalently attached to the
CC adiponectin polypeptide. The adiponectin polypeptide comprises an amino
CC acid residue having an attachment group for the first non-polypeptide
CC moiety which has been introduced in a position where the parent
CC adiponectin is occupied by a surface exposed amino acid residue. The
CC conjugate of the invention demonstrates antiarteriosclerotic,
CC antidiabetic, cardiant, antirheumatic, antibacterial, antilipemic,
CC dermatological, immunosuppressive, immunomodulator and anorectic
CC activities and may be useful for treating diabetes, obesity,
CC atherosclerosis, cardiovascular diseases, dyslipidaemia, rheumatoid
CC arthritis, Crohn's disease, systemic lupus erythematosus, Sjogren
CC syndrome, cachexia, septic shock, myasthenia gravis, myocardial
CC infarction and destructive processes related to activation of the
CC inflammatory system, as well as during gene therapy procedures. The
CC current sequence is that of the human adiponectin apM1 (82-244) mutant
CC protein of the invention.
XX
XX
SQ Sequence 163 AA;
Query Match 100.0%; Score 708; DB 7; Length 163;
Best Local Similarity 100.0%; Pred. No. 4.8e-76;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FSVGLETVVTIPNMPRIPTKIFYNQNHVDSGTFKHCNIPGLYFAVHITVYMKDVVS 60
DB 34 FSVGLETVVTIPNMPRIPTKIFYNQNHVDSGTFKHCNIPGLYFAVHITVYMKDVVS 93
QY 61 LFKKDKAMLFYTDYOENNVDOAGSVLLHLEVGDQVWLQYGGEBRNGLYADNDNDSTF 120
DB 94 LFKKDKAMLFYTDYOENNVDOAGSVLLHLEVGDQVWLQYGGEBRNGLYADNDNDSTF 153
QY 121 TGFLLYHDTN 130
DB 154 TGFLLYHDTN 163
RESULT 9
ADE93615
ID ADE93615 standard; protein; 187 AA.
AC ADE93615;
XX
XX
DT 12-FEB-2004 (first entry)
DE
XX
XX
XX Human adiponectin apM1 (58-244) protein.
KM adiponectin conjugate; antiarteriosclerotic; antidiabetic; cardiant;
KM antirheumatic; antibacterial; antilipemic; dermatological;

KM immunosuppressive; immunomodulator; anorectic; diabetes; obesity;
KM atherosclerosis; cardiovascular disease; dyslipidaemia;
KM rheumatoid arthritis; Crohn's; systemic lupus erythematosus;
KM Sjogren syndrome; cachexia; septic shock; myasthenia gravis;
KM myocardial infarction; inflammation; gene therapy; human; apM1;
KM wild-type.
XX
XX
OS Homo sapiens.
XX
XX
PN WO2003055916-A2.
XX
XX
PD 10-JUL-2003.
XX
XX
PF 20-DEC-2002; 2002WO-DK000897.
XX
XX
PR 21-DEC-2001; 2001DK-00001952.
PR 21-DEC-2001; 2001US-0343482P.
PR 25-APR-2002; 2002DK-0000627.
PR 25-APR-2002; 2002US-0375492P.
PR 03-JUL-2002; 2002DK-00001036.
PR 03-JUL-2002; 2002US-0394117P.
PR 20-SEP-2002; 2002DK-00001385.
PR 20-SEP-2002; 2002US-0412169P.
XX
XX
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
XX
XX
PI Rasmussen PB, Andersen KV, Pedersen AH, Schambye HT, Halkier T;
PI Bogenes A;
XX
XX
DR MPI: 2003-598262/56.
DR N-PSDB; ADE93617.
XX
XX
PT New conjugate comprising an adiponectin polypeptide and a first non-
PT polypeptide moiety, useful for preparing a composition for treating a
PT mammal having e.g., diabetes, atherosclerosis or cardiovascular disease.
XX
XX
PS Claim 44; SEQ ID NO 13; 184bp; English.
XX
XX
CC The invention relates to a novel conjugate comprising an adiponectin
CC polypeptide and a first non-polypeptide moiety covalently attached to the
CC adiponectin polypeptide. The adiponectin polypeptide comprises an amino
CC acid residue having an attachment group for the first non-polypeptide
CC moiety which has been introduced in a position where the parent
CC adiponectin is occupied by a surface exposed amino acid residue. The
CC conjugate of the invention demonstrates antiarteriosclerotic,
CC antidiabetic, cardiant, antirheumatic, antibacterial, antilipemic,
CC dermatological, immunosuppressive, immunomodulator and anorectic
CC activities and may be useful for treating diabetes, obesity,
CC atherosclerosis, cardiovascular diseases, dyslipidaemia, rheumatoid
CC arthritis, Crohn's disease, systemic lupus erythematosus, Sjogren
CC syndrome, cachexia, septic shock, myasthenia gravis, myocardial
CC infarction and destructive processes related to activation of the
CC inflammatory system, as well as during gene therapy procedures. The
CC current sequence is that of the human adiponectin apM1 protein of the
CC invention.
XX
XX
SQ Sequence 187 AA;
Query Match 100.0%; Score 708; DB 7; Length 187;
Best Local Similarity 100.0%; Pred. No. 5.8e-78;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FSVGLETVVTIPNMPRIPTKIFYNQNHVDSGTFKHCNIPGLYFAVHITVYMKDVVS 60
DB 58 FSVGLETVVTIPNMPRIPTKIFYNQNHVDSGTFKHCNIPGLYFAVHITVYMKDVVS 117
QY 61 LFKKDKAMLFYTDYOENNVDOAGSVLLHLEVGDQVWLQYGGEBRNGLYADNDNDSTF 120
DB 118 LFKKDKAMLFYTDYOENNVDOAGSVLLHLEVGDQVWLQYGGEBRNGLYADNDNDSTF 177
QY 121 TGFLLYHDTN 130

Db 178 TGFLYHDTN 187

RESULT 10

AD93614 ID ADE93614 standard; protein; 193 AA.

XX AC ADE93614;

XX DT 12-FEB-2004 (first entry)

XX DE Human adiponectin apM1(52-244) protein.

XX KM adiponectin conjugate; antiarteriosclerotic; antidiabetic; cardiant; antirheumatic; antibacterial; antilipaeamic; dermatological; immunosuppressive; immunomodulator; anorectic; diabetes; obesity; atherosclerosis; cardiovascular disease; dyslipidaemia; rheumatoid arthritis; Crohn's; systemic lupus erythematosus; Sjogren syndrome; cachexia; septic shock; myasthenia gravis; myocardial infarction; inflammation; gene therapy; human; apM1; wild-type.

XX KM Homo sapiens.

OS Homo sapiens.

XX PN WO2003055916-A2.

XX PD 10-JUL-2003.

XX PF 20-DEC-2002; 2002WO-DK000897.

XX PR 21-DEC-2001; 2001DK-00001952.

XX PR 21-DEC-2001; 2001US-0343482P.

XX PR 25-APR-2002; 2002DK-00000627.

XX PR 25-APR-2002; 2002US-0375492P.

XX PR 03-JUL-2002; 2002DK-00001036.

XX PR 03-JUL-2002; 2002US-0394117P.

XX PR 20-SEP-2002; 2002DK-00001385.

XX PR 20-SEP-2002; 2002US-0412169P.

XX PA (MAXY-) MAXYGEN APS.

XX PA (MAXY-) MAXYGEN HOLDINGS LTD.

XX PI Rasmussen PB, Andersen KV, Pedersen AH, Schambye HT, Halkier T; Bognes A;

XX DR WPI; 2003-598262/56.

XX DR N-PSDB; ADE93616.

XX PT New conjugate comprising an adiponectin polypeptide and a first non-polypeptide moiety, useful for preparing a composition for treating a mammal having e.g., diabetes, atherosclerosis or cardiovascular disease.

XX PS Claim 44; SEQ ID NO 12; 184pp; English.

XX CC The invention relates to a novel conjugate comprising an adiponectin polypeptide and a first non-polypeptide moiety covalently attached to the acid residue having an attachment group for the first non-polypeptide moiety which has been introduced in a position where the parent adiponectin is occupied by a surface exposed amino acid residue. The conjugate of the invention demonstrates antiarteriosclerotic, antidiabetic, cardiant, antirheumatic, antibacterial, antilipaeamic, dermatological, immunosuppressive, immunomodulator and anorectic activities and may be useful for treating diabetes, obesity, atherosclerosis, cardiovascular diseases, dyslipidaemia, rheumatoid arthritis, Crohn's disease, systemic lupus erythematosus, Sjogren syndrome, cachexia, septic shock, myasthenia gravis, myocardial infarction and destructive processes related to activation of the inflammatory system, as well as during gene therapy procedures. The current sequence is that of the human adiponectin apM1 protein of the invention.

XX CC Sequence 193 AA;

XX SO

Query Match 100.0%; Score 708; DB 7; Length 193;

Best Local Similarity 100.0%; Pred. No. 6, 1e-78;

Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSVGLTETVYTIIPMPRIPTKIFPNQNHVDSGTGKFKCNIPGLYFAYHITVYMKDVKS 60

DB 64 PSVGLTETVYTIIPMPRIPTKIFPNQNHVDSGTGKFKCNIPGLYFAYHITVYMKDVKS 123

QY 61 LFKKDKAMLPYDQYQENNVDASGSVLLHLEVGDDVWLOVYGEGERNGLYANDNDSTF 120

DB 124 LFKKDKAMLPYDQYQENNVDASGSVLLHLEVGDDVWLOVYGEGERNGLYANDNDSTF 183

QY 121 TGFLYHDTN 130

DB 184 TGFLYHDTN 193

RESULT 11

AD93605 ID ADE93605 standard; protein; 203 AA.

XX AC ADE93605;

XX DT 12-FEB-2004 (first entry)

XX DE Human adiponectin apM1(42-244) protein.

XX KM adiponectin conjugate; antiarteriosclerotic; antidiabetic; cardiant; antirheumatic; antibacterial; antilipaeamic; dermatological; immunosuppressive; immunomodulator; anorectic; diabetes; obesity; atherosclerosis; cardiovascular disease; dyslipidaemia; rheumatoid arthritis; Crohn's; systemic lupus erythematosus; Sjogren syndrome; cachexia; septic shock; myasthenia gravis; myocardial infarction; inflammation; gene therapy; human; apM1; wild-type.

XX KM Homo sapiens.

OS Homo sapiens.

XX PN WO2003055916-A2.

XX PD 10-JUL-2003.

XX PF 20-DEC-2002; 2002WO-DK000897.

XX PR 21-DEC-2001; 2001DK-00001952.

XX PR 21-DEC-2001; 2001US-0343482P.

XX PR 25-APR-2002; 2002DK-00000627.

XX PR 25-APR-2002; 2002US-0375492P.

XX PR 03-JUL-2002; 2002DK-00001036.

XX PR 03-JUL-2002; 2002US-0394117P.

XX PR 20-SEP-2002; 2002DK-00001385.

XX PR 20-SEP-2002; 2002US-0412169P.

XX PA (MAXY-) MAXYGEN APS.

XX PA (MAXY-) MAXYGEN HOLDINGS LTD.

XX PI Rasmussen PB, Andersen KV, Pedersen AH, Schambye HT, Halkier T; Bognes A;

XX DR WPI; 2003-598262/56.

XX PT New conjugate comprising an adiponectin polypeptide and a first non-polypeptide moiety, useful for preparing a composition for treating a mammal having e.g., diabetes, atherosclerosis or cardiovascular disease.

XX PS Claim 44; SEQ ID NO 3; 184pp; English.

XX CC The invention relates to a novel conjugate comprising an adiponectin polypeptide and a first non-polypeptide moiety covalently attached to the acid residue having an attachment group for the first non-polypeptide moiety which has been introduced in a position where the parent

CC adiponectin is occupied by a surface exposed amino acid residue. The
CC conjugate of the invention demonstrates antiarteriosclerotic.
CC antidiabetic, cardiant, antirheumatic, antibacterial, antilipemic,
CC dermatological, immunosuppressive, immunomodulator and anorectic
CC activities and may be useful for treating diabetes, obesity,
CC atherosclerosis, cardiovascular diseases, dyslipidaemia, rheumatoid
CC arthritis, Crohn's disease, systemic lupus erythematosus, Sjogren
CC syndrome, cachexia, septic shock, myasthenia gravis, myocardial
CC infarction and destructive processes related to activation of the
CC inflammatory system, as well as during gene therapy procedures. The
CC current sequence is that of the human adiponectin apM1 protein of the
CC invention.

CC Sequence 203 AA;

Query Match 100.0%; Score 708; DB 7; Length 203;
Best Local Similarity 100.0%; Pred. No. 6.5e-78;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSVGLETVVTPNMPIRFTKIFVNOQNHVDSGTFKHCNIPGLYFAVHITVYMKDVYS 60
DB 74 FSVGLETVVTPNMPIRFTKIFVNOQNHVDSGTFKHCNIPGLYFAVHITVYMKDVYS 133
QY 61 LFKDKKAMLFYYDQYQENNVDAAGSVLLHLEVGDPQWLQYVGGERNGLYADNDNDSTF 120
DB 134 LFKDKKAMLFYYDQYQENNVDAAGSVLLHLEVGDPQWLQYVGGERNGLYADNDNDSTF 193

QY 121 TGFLLYHDTN 130
DB 194 TGFLLYHDTN 203

RESULT 12
ADE93604
ID ADE93604 standard; protein; 226 AA.

AC ADE93604;

DT 12-FEB-2004 (first entry)

DE Human adiponectin apM1 (19-244) protein.

XX adiponectin conjugate; antiarteriosclerotic; antidiabetic; cardiant;
KW antirheumatic; antibacterial; antilipemic; dermatological;
KW immunosuppressive; immunomodulator; anorectic; diabetes; obesity;
KW atherosclerosis; cardiovascular disease; dyslipidaemia;
KW rheumatoid arthritis; Crohn's; systemic lupus erythematosus;
KW Sjogren syndrome; cachexia; septic shock; myasthenia gravis;
KW myocardial infarction; inflammation; gene therapy; human; apM1;
KW wild-type.

XX Homo sapiens.

OS WO2003055916-A2.

XX 10-JUL-2003.

PD 20-DEC-2002; 2002WO-DK000897.

XX 21-DEC-2001; 2001DK-00001952.
PR 21-DEC-2001; 2001US-0343482P.
PR 25-APR-2002; 2002DK-00000627.
PR 25-APR-2002; 2002US-0375492P.
PR 03-JUL-2002; 2002DK-00001036.
PR 03-JUL-2002; 2002US-0394117P.
PR 20-SEP-2002; 2002DK-00001385.
PR 20-SEP-2002; 2002US-0412169P.

XX (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.

XX Rasmussen PB, Andersen KV, Pedersen AH, Schambye HT, Halkier T;
PI Bogense A;

XX WPI; 2003-598262/56.

DR New conjugate comprising an adiponectin polypeptide and a first non-
XX polypeptide moiety, useful for preparing a composition for treating a
PT mammal having e.g., diabetes, atherosclerosis or cardiovascular disease.

PS Claim 14; SEQ ID NO 2; 184bp; English.

XX The invention relates to a novel conjugate comprising an adiponectin
CC polypeptide and a first non-polypeptide moiety covalently attached to the
CC adiponectin polypeptide. The adiponectin polypeptide comprises an amino
CC acid residue having an attachment group for the first non-polypeptide
CC moiety which has been introduced in a position where the parent
CC adiponectin is occupied by a surface exposed amino acid residue. The
CC conjugate of the invention demonstrates antiarteriosclerotic.
CC antidiabetic, cardiant, antirheumatic, antibacterial, antilipemic,
CC dermatological, immunosuppressive, immunomodulator and anorectic
CC activities and may be useful for treating diabetes, obesity,
CC atherosclerosis, cardiovascular diseases, dyslipidaemia, rheumatoid
CC arthritis, Crohn's disease, systemic lupus erythematosus, Sjogren
CC syndrome, cachexia, septic shock, myasthenia gravis, myocardial
CC infarction and destructive processes related to activation of the
CC inflammatory system, as well as during gene therapy procedures. The
CC current sequence is that of the human adiponectin apM1 protein of the
CC invention.

SQ Sequence 226 AA;

Query Match 100.0%; Score 708; DB 7; Length 226;
Best Local Similarity 100.0%; Pred. No. 7.5e-78;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSVGLETVVTPNMPIRFTKIFVNOQNHVDSGTFKHCNIPGLYFAVHITVYMKDVYS 60
DB 97 FSVGLETVVTPNMPIRFTKIFVNOQNHVDSGTFKHCNIPGLYFAVHITVYMKDVYS 156

QY 61 LFKDKKAMLFYYDQYQENNVDAAGSVLLHLEVGDPQWLQYVGGERNGLYADNDNDSTF 120
DB 157 LFKDKKAMLFYYDQYQENNVDAAGSVLLHLEVGDPQWLQYVGGERNGLYADNDNDSTF 216

QY 121 TGFLLYHDTN 130
DB 217 TGFLLYHDTN 226

RESULT 13
AAV21808
ID AAV21808 standard; protein; 231 AA.

AC AAV21808;

DT 10-SEP-1999 (first entry)

DE Adipose most abundant gene transcription product 1 (apM1) fragment.

XX Smooth muscle proliferation; secretion factor; apM1; adipose;
KW adipose most abundant gene transcription product 1; obesity;
KW arteriosclerosis; restenosis; angina pectoris; myocardial infarction.

XX Unidentified.

OS WO9921577-A1.

XX 06-MAY-1999.

PD 27-OCT-1998; 98WO-JP004862.

PR 29-OCT-1997; 97JP-00297569.

PA (SAXA) OTSUKA PHARM CO LTD.

XX Matsuzawa Y, Ohmoto Y;

XX WPI; 1999-418412/35.
XX
XX Inhibition of smooth muscle proliferation using secretion factor apM1.
PT
XX Example; Page 59-60; 65pp; Japanese.
XX
CC Then invention relates to the inhibition of smooth muscle proliferation
CC using a composition containing secretion factor apM1 (adipose most
CC abundant gene transcript product 1), together with a suitable carrier.
CC apM1 is expressed specifically in adipose tissue and the composition is
CC used for the prevention and treatment of arteriosclerosis; restenosis
CC following vascular reconstruction; and treatment and diagnosis of
CC diseases related to obesity, and disorders associated with it such as
CC angina pectoris and myocardial infarction. The present sequence
CC represents a fragment of apM1 isolated from abdominal fat tissue of myoma
CC uteri
XX
SQ Sequence 231 AA:
XX
Query Match 100.0%; Score 708; DB 2; Length 231;
Best Local Similarity 100.0%; Pred. No. 7, 8e-78;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FSVGLETVYTIIPMPPIRFTKIFYNQNNHYDGSFGKFCNIPGLYFAYHITVYMKDVKS 60
DB 102 FSVGLETVYTIIPMPPIRFTKIFYNQNNHYDGSFGKFCNIPGLYFAYHITVYMKDVKS 161
QY 61 LFKKDXAMLFTYDQYQENNVDAQSGSVLHLLEVGDQVWLQVYGEGERNGLYADNDSTF 120
DB 162 LFKKDXAMLFTYDQYQENNVDAQSGSVLHLLEVGDQVWLQVYGEGERNGLYADNDSTF 221
QY 121 TGFLLYHDTN 130
DB 222 TGFLLYHDTN 231
XX
RESULT 14
AAB60347
ID AAB60347 standard; protein; 231 AA.
XX
XX AAB60347;
AC
XX
DT 06-APR-2001 (first entry)
XX
DE Recombinant human apM1 protein (residues 15-244 + Met1), SEQ ID NO:3.
XX
XX Antigenic protein detection; sodium sulphate; ELISA;
KM enzyme-linked immunosorbent assay; human apM1; recombinant expression;
KM Escherichia coli; adipose most abundant gene transcript 1;
KM adipose-specific collagen-like factor.
XX
XX Homo sapiens.
OS Synthetic.
OS
XX JP2000304748-A.
PN
XX
XX 02-NOV-2000.
PD
XX
XX 21-APR-1999; 99JP-00114170.
PF
XX
XX 21-APR-1999; 99JP-00114170.
PR
XX
XX (SAKA) OTSUKA PHARM CO LTD.
PA
XX
XX WPI; 2001-127687/14.
DR
XX
XX Detection of an antigenic protein comprises use of enzyme linked
PT immunosorbant assay.
PT
XX Example 1; Page 7-8; 10pp; Japanese.
PS
XX
CC The invention relates to a method for detecting an antigenic protein. The

CC method comprises boiling the sample containing the antigenic protein in
CC the presence of sodium sulphate, diluting it in buffer, and detecting the
CC enzyme by enzyme-linked immunosorbent assay (ELISA). In an
CC exemplification of the invention, residues 15-244 (plus an initial Met
CC residue) of human apM1 (adipose most abundant gene transcript 1;
CC AAB60347), an adipose-specific collagen-like factor, was recombinantly
CC expressed in Escherichia coli. Using the method of the invention, it was
CC found that apM1 was expressed mainly in the inclusion body fragment as an
CC approximately 30 kd protein. The present sequence represents the
CC recombinantly expressed human apM1
XX
SQ Sequence 231 AA:
XX
Query Match 100.0%; Score 708; DB 4; Length 231;
Best Local Similarity 100.0%; Pred. No. 7, 8e-78;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FSVGLETVYTIIPMPPIRFTKIFYNQNNHYDGSFGKFCNIPGLYFAYHITVYMKDVKS 60
DB 102 FSVGLETVYTIIPMPPIRFTKIFYNQNNHYDGSFGKFCNIPGLYFAYHITVYMKDVKS 161
QY 61 LFKKDXAMLFTYDQYQENNVDAQSGSVLHLLEVGDQVWLQVYGEGERNGLYADNDSTF 120
DB 162 LFKKDXAMLFTYDQYQENNVDAQSGSVLHLLEVGDQVWLQVYGEGERNGLYADNDSTF 221
QY 121 TGFLLYHDTN 130
DB 222 TGFLLYHDTN 231
XX
RESULT 15
ADD93530
ID ADD93530 standard; protein; 233 AA.
XX
XX ADD93530;
AC
XX
DT 29-JAN-2004 (first entry)
XX
DE Novel NOV2e, homologous to human adiponectin.
XX
XX NOV2e; human; adiponectin; gene therapy.
KM
XX
XX Homo sapiens.
OS
XX
XX WO2003078572-A2.
PN
XX
XX 25-SEP-2003.
PD
XX
XX 06-MAR-2003; 2003WO-US006859.
PF
XX
XX 15-MAR-2002; 2002US-0365034P.
PR
XX
XX 19-MAR-2002; 2002US-0365477P.
PR
XX
XX 21-MAR-2002; 2002US-0366420P.
PR
XX
XX 05-MAR-2003; 2003US-00379747.
XX
XX (CURA-) CURAGEN CORP.
PA
XX
XX Burgess CE, Chant JS, Chaudhuri A, Edinger SR, Gangoli EA;
PI Malyanekar UM, Miller CE, Ooi CE, Ort T, Paturajan M, Raetelli L;
PI Rieger DK, Shinkets RA, Zehusen BD;
PI
XX
XX WPI; 2003-779122/73.
DR
XX
XX N-PSDB; ADD93529.
DR
XX
XX
XX
XX New isolated NOVX polypeptides and polynucleotides, useful for
PT preventing, diagnosing or treating NOVX-associated disorders, e.g.
PT osteoarthritis, obesity, arteriosclerosis, cancer, Parkinson's disease,
PT asthma, or infections.
XX
XX Claim 1; Page 108; 205pp; English.
PS
XX
XX The present sequence is the protein sequence of a novel polypeptide,
CC designated NOV2e, that shows amino acid sequence homology to the human

CC adiponectin (adipose most abundant gene transcript 1, APM1). The
 CC adiponectin gene is the most abundant gene transcript in adipose cells
 CC that regulate lipid metabolism. An interaction between adiponectin and
 CC calcium modulating ligand was identified, indicating a novel pathway by
 CC which adiponectin may induce lipid breakdown in muscle cells and
 CC adipocytes. The invention is based on the identification of proteins and
 CC polypeptides, and the nucleic acids encoding them, that are
 CC differentially modulated in a pathological state, disease or an abnormal
 CC condition or state. These are targets for therapeutic agents and can be
 CC used in screening methodologies to identify candidate therapeutic agents
 CC which interact with the target and thereby exert a desired or favourable
 CC effect, e.g. in neurogenesis, cell differentiation, cell proliferation,
 CC haematopoiesis, wound healing and angiogenesis. Methods for diagnosis,
 CC treatment and prevention of disorders involving the novel human nucleic
 CC acids and proteins are provided. The polypeptides are also used to raise
 CC antibodies, useful in therapy and diagnosis.

CC
 XX
 SQ Sequence 233 AA;

Query Match 100.0%; Score 708; DB 7; Length 233;
 Best Local Similarity 100.0%; Pred. No. 7.9e-76;
 Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB	104	FSVGLTETVTIPNMP	IRFTKIFYNQ	QNHGSGTGK	FCNIPGLYYFAYHITVYMKDV	KVS 163
QY	61	LFKKDKAMLFYDQYQENN	VDAGSGVLHLE	VGQVWLQYV	GEGERNGLYADND	STF 120
DB	164	LFKKDKAMLFYDQYQENN	VDAGSGVLHLE	VGQVWLQYV	GEGERNGLYADND	STF 223
QY	121	TGFLLYHDTN	130			
DB	224	TGFLLYHDTN	233			

Search completed: May 6, 2005, 17:22:12
 Job time : 79.0651 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 8, 2005, 13:27:58 ; Search time 55.967 Seconds

(without alignments)
774.883 Million cell updates/sec

Title: US-10-072-159-11

Perfect score: 708

Sequence: 1 FSVGLETVYTIMPMPIRFTK.....YADNDNDSTFTGFLYHDTN 130

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1428581 seqs, 33359853 residues

Total number of hits satisfying chosen parameters: 1428581

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:
1: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubppaa/US06_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubppaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubppaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep:*
8: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB.pep:*
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19: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	708	100.0	130	13	US-10-072-159-11
2	708	100.0	130	13	US-10-060-845-11
3	708	100.0	130	14	US-10-325-717-7
4	708	100.0	137	14	US-10-325-717-6
5	708	100.0	144	14	US-10-325-717-5
6	708	100.0	145	14	US-10-325-717-4
7	708	100.0	157	14	US-10-325-717-3
8	708	100.0	160	17	US-10-659-782A-23
9	708	100.0	163	14	US-10-325-717-10
10	708	100.0	163	14	US-10-325-717-10
11	708	100.0	187	14	US-10-325-717-53
12	708	100.0	193	14	US-10-325-717-12
13	708	100.0	203	14	US-10-325-717-3

14	708	100.0	226	14	US-10-325-717-2	Sequence 2, Appl1
15	708	100.0	231	14	US-10-189-493-2	Sequence 2, Appl1
16	708	100.0	233	15	US-10-379-747-14	Sequence 14, Appl1
17	708	100.0	244	9	US-09-776-976-6	Sequence 6, Appl1
18	708	100.0	244	9	US-09-758-055-6	Sequence 6, Appl1
19	708	100.0	244	9	US-09-509-547-6	Sequence 6, Appl1
20	708	100.0	244	9	US-09-911-1768-48	Sequence 48, Appl1
21	708	100.0	244	14	US-10-180-762-51	Sequence 51, Appl1
22	708	100.0	244	14	US-10-231-814-6	Sequence 6, Appl1
23	708	100.0	244	14	US-10-234-000-4	Sequence 4, Appl1
24	708	100.0	244	14	US-10-360-186-51	Sequence 51, Appl1
25	708	100.0	244	14	US-10-321-164-3	Sequence 3, Appl1
26	708	100.0	244	14	US-10-376-460-6	Sequence 6, Appl1
27	708	100.0	244	14	US-10-189-493-1	Sequence 1, Appl1
28	708	100.0	244	14	US-10-197-293-3	Sequence 3, Appl1
29	708	100.0	244	14	US-10-325-717-1	Sequence 1, Appl1
30	708	100.0	244	15	US-10-411-120-67	Sequence 67, Appl1
31	708	100.0	244	15	US-10-379-747-6	Sequence 6, Appl1
32	708	100.0	244	15	US-10-379-747-8	Sequence 8, Appl1
33	708	100.0	244	15	US-10-379-747-10	Sequence 10, Appl1
34	708	100.0	244	15	US-10-621-787-3	Sequence 3, Appl1
35	708	100.0	244	15	US-10-283-833-6	Sequence 6, Appl1
36	708	100.0	244	17	US-10-676-790-4	Sequence 4, Appl1
37	708	100.0	244	17	US-10-487-039-1	Sequence 1, Appl1
38	708	100.0	244	17	US-10-775-180-681	Sequence 681, Appl1
39	708	100.0	244	17	US-10-775-180-682	Sequence 682, Appl1
40	708	100.0	244	17	US-10-659-782A-22	Sequence 22, Appl1
41	708	100.0	244	17	US-10-970-648-6	Sequence 6, Appl1
42	708	100.0	244	17	US-10-492-179-22	Sequence 22, Appl1
43	708	100.0	244	17	US-10-495-317-6	Sequence 6, Appl1
44	708	100.0	250	15	US-10-379-747-12	Sequence 12, Appl1
45	708	100.0	250	15	US-10-379-747-12	Sequence 12, Appl1

ALIGNMENTS

RESULT 1
US-10-072-159-11
Sequence 11, Application US/10072159
Public Information No. US20020151498A1
GENERAL INFORMATION:
APPLICANT: Bihaud, Bernard
APPLICANT: Bouguieret, Lydie
APPLICANT: Yen-Potin, Frances
TITLE OF INVENTION: Lipoprotein-regulating medicaments
FILE REFERENCE: GENSET. 036APC
CURRENT APPLICATION NUMBER: US/10/072,159
CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: 09/485,316
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: FR 98/05032
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: PCT IB98/01256
PRIOR FILING DATE: 1998-08-06
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patent.pm
SEQ ID NO 11
LENGTH: 130
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIMILAR
LOCATION: 1..130
OTHER INFORMATION: Fragment 115..244 of translation from ref Genbank D45371
US-10-072-159-11

Query Match 100.0%; Score 708; DB 13; Length 130;
Best Local Similarity 100.0%; Pred. No. 4.4e-70;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 FSVGLETVYTIMPMPIRFTKIFYNQONHYDSGTGFCNIPGLYYFAVHITVYMKDVKS 60
|||||

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Db 1 FSVGLETVITIPNMPIRFTKIFYNQNNHYDSTGKFCNIPGLYFFAYHITVYMKDVKS 60
Qy 61 LFKDKKAMLFYDYQOENNVDQASGVLHLLEVGDQWMLQYVGEGERNGLYADNDNDSTF 120
Db 61 LFKDKKAMLFYDYQOENNVDQASGVLHLLEVGDQWMLQYVGEGERNGLYADNDNDSTF 120
Qy 121 TGFLLYHDTN 130
Db 121 TGFLLYHDTN 130

RESULT 2
US-10-060-845-11
; Sequence 11, Application US/10060845
; Publication No. US20020165154A1
; GENERAL INFORMATION:
; APPLICANT: Bihain, Bernard
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Yen-Potin, Frances
; TITLE OF INVENTION: Lipoprotein-regulating medicaments
; FILE REFERENCE: GENSET.03CAPC
; CURRENT APPLICATION NUMBER: US/10/060,845
; PRIOR FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: U.S. 09/485,316
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: FR 97/10088
; PRIOR FILING DATE: 1997-08-06
; PRIOR APPLICATION NUMBER: FR 98/05032
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: PCT IB98/01256
; PRIOR FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent.pm
; SEQ ID NO 11
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: 1..130
; OTHER INFORMATION: fragment 115..244 of translation from ref Genbank D45371
US-10-060-845-11

Query Match 100.0%; Score 708; DB 13; Length 130;
Best Local Similarity 100.0%; Pred. No. 4.4e-70;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FSVGLETVITIPNMPIRFTKIFYNQNNHYDSTGKFCNIPGLYFFAYHITVYMKDVKS 60
Db 1 FSVGLETVITIPNMPIRFTKIFYNQNNHYDSTGKFCNIPGLYFFAYHITVYMKDVKS 60
Qy 61 LFKDKKAMLFYDYQOENNVDQASGVLHLLEVGDQWMLQYVGEGERNGLYADNDNDSTF 120
Db 61 LFKDKKAMLFYDYQOENNVDQASGVLHLLEVGDQWMLQYVGEGERNGLYADNDNDSTF 120
Qy 121 TGFLLYHDTN 130
Db 121 TGFLLYHDTN 130

RESULT 3
US-10-325-717-7
; Sequence 7, Application US/10325717
; Publication No. US20030176328A1
; GENERAL INFORMATION:
; APPLICANT: Rasmussen, Poul Baad
; APPLICANT: Andersen, Kim Vilbourn
; APPLICANT: Pedersen, Anders Hjelholt
; APPLICANT: Schambye, Hans Thalsgaard
; APPLICANT: Halkier, Torben
; APPLICANT: Bognes, Are
; TITLE OF INVENTION: Adiponectin Fragments and Conjugates
; FILE REFERENCE: 0251us610
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; CURRENT APPLICATION NUMBER: US/10/325,717
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/412,169
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US 60/394,117
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/375,492
; PRIOR FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US 60/343,482
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: apM1(115-244)
US-10-325-717-7

Query Match 100.0%; Score 708; DB 14; Length 130;
Best Local Similarity 100.0%; Pred. No. 4.4e-70;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FSVGLETVITIPNMPIRFTKIFYNQNNHYDSTGKFCNIPGLYFFAYHITVYMKDVKS 60
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Qy 61 LFKDKKAMLFYDYQOENNVDQASGVLHLLEVGDQWMLQYVGEGERNGLYADNDNDSTF 120
Db 61 LFKDKKAMLFYDYQOENNVDQASGVLHLLEVGDQWMLQYVGEGERNGLYADNDNDSTF 120
Qy 121 TGFLLYHDTN 130
Db 121 TGFLLYHDTN 130

RESULT 4
US-10-325-717-6
; Sequence 6, Application US/10325717
; Publication No. US20030176328A1
; GENERAL INFORMATION:
; APPLICANT: Rasmussen, Poul Baad
; APPLICANT: Andersen, Kim Vilbourn
; APPLICANT: Pedersen, Anders Hjelholt
; APPLICANT: Schambye, Hans Thalsgaard
; APPLICANT: Halkier, Torben
; APPLICANT: Bognes, Are
; TITLE OF INVENTION: Adiponectin Fragments and Conjugates
; FILE REFERENCE: 0251us610
; CURRENT APPLICATION NUMBER: US/10/325,717
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/412,169
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US 60/394,117
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/375,492
; PRIOR FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US 60/343,482
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: apM1(108-244)
US-10-325-717-6

Query Match 100.0%; Score 708; DB 14; Length 137;
Best Local Similarity 100.0%; Pred. No. 4.7e-70;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 FSVGLETTYVTIPNMPIRFTKIFYNQONHYDGSYGKPHCNIPGLYYFAYHITVYMKDVKS 60
      8 FSVGLETTYVTIPNMPIRFTKIFYNQONHYDGSYGKPHCNIPGLYYFAYHITVYMKDVKS 67
Db      61 LFKKDKAMLETTYQOYENNVDAQSGSVLLHLEVGDDQVWLQVYGEGERNGLYANDNDSTF 120
      68 LFKKDKAMLETTYQOYENNVDAQSGSVLLHLEVGDDQVWLQVYGEGERNGLYANDNDSTF 127
QY      121 TGFLLYHDTN 130
      128 TGFLLYHDTN 137
Db

RESULT 5
US-10-325-717-5
; Sequence 5, Application US/10325717
; Publication No. US20030176328A1
; GENERAL INFORMATION:
; APPLICANT: Raemussen, Poul Baad
; APPLICANT: Andersen, Kim Vilbour
; APPLICANT: Pedersen, Anders Hjelholt
; APPLICANT: Schambye, Hans Thalsgaard
; APPLICANT: Halkier, Torben
; APPLICANT: Bognes, Are
; TITLE OF INVENTION: Adiponectin Fragments and Conjugates
; FILE REFERENCE: 0251us610
; CURRENT APPLICATION NUMBER: US/10/325,717
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/412,169
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US 60/394,117
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/375,492
; PRIOR FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US 60/343,482
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: apM1(101-244)
US-10-325-717-5

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QY      1 FSVGLETTYVTIPNMPIRFTKIFYNQONHYDGSYGKPHCNIPGLYYFAYHITVYMKDVKS 60
      15 FSVGLETTYVTIPNMPIRFTKIFYNQONHYDGSYGKPHCNIPGLYYFAYHITVYMKDVKS 74
Db      61 LFKKDKAMLETTYQOYENNVDAQSGSVLLHLEVGDDQVWLQVYGEGERNGLYANDNDSTF 120
      75 LFKKDKAMLETTYQOYENNVDAQSGSVLLHLEVGDDQVWLQVYGEGERNGLYANDNDSTF 134
QY      121 TGFLLYHDTN 130
      135 TGFLLYHDTN 144
Db

RESULT 6
US-10-325-717-11
; Sequence 11, Application US/10325717
; Publication No. US20030176328A1
; GENERAL INFORMATION:
; APPLICANT: Raemussen, Poul Baad
; APPLICANT: Andersen, Kim Vilbour
; APPLICANT: Pedersen, Anders Hjelholt
; APPLICANT: Schambye, Hans Thalsgaard
```

```
; APPLICANT: Halkier, Torben
; APPLICANT: Bognes, Are
; TITLE OF INVENTION: Adiponectin Fragments and Conjugates
; FILE REFERENCE: 0251us610
; CURRENT APPLICATION NUMBER: US/10/325,717
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/412,169
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US 60/394,117
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/375,492
; PRIOR FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US 60/343,482
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: apM1(100-244)
US-10-325-717-11

Query Match      100.0%; Score 708; DB 14; Length 145;
Best Local Similarity 100.0%; Pred. No. 5e-70; Indels 0; Gaps 0;
Matches 130; Conservative 0; Mismatches 0;

QY      1 FSVGLETTYVTIPNMPIRFTKIFYNQONHYDGSYGKPHCNIPGLYYFAYHITVYMKDVKS 60
      16 FSVGLETTYVTIPNMPIRFTKIFYNQONHYDGSYGKPHCNIPGLYYFAYHITVYMKDVKS 75
Db      61 LFKKDKAMLETTYQOYENNVDAQSGSVLLHLEVGDDQVWLQVYGEGERNGLYANDNDSTF 120
      76 LFKKDKAMLETTYQOYENNVDAQSGSVLLHLEVGDDQVWLQVYGEGERNGLYANDNDSTF 135
QY      121 TGFLLYHDTN 130
      136 TGFLLYHDTN 145
Db

RESULT 7
US-10-325-717-4
; Sequence 4, Application US/10325717
; Publication No. US20030176328A1
; GENERAL INFORMATION:
; APPLICANT: Raemussen, Poul Baad
; APPLICANT: Andersen, Kim Vilbour
; APPLICANT: Pedersen, Anders Hjelholt
; APPLICANT: Schambye, Hans Thalsgaard
; APPLICANT: Halkier, Torben
; APPLICANT: Bognes, Are
; TITLE OF INVENTION: Adiponectin Fragments and Conjugates
; FILE REFERENCE: 0251us610
; CURRENT APPLICATION NUMBER: US/10/325,717
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/412,169
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US 60/394,117
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/375,492
; PRIOR FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US 60/343,482
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: apM1(88-244)
US-10-325-717-4
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Best Local Similarity 100.0%; Pred. No. 5.5e-70;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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    |||||
Db 28 FSVGLETVVTIPNMPIRFTKIFYNQONHYDSTGKFGHCNIPGLYFAVHITVYMKDVKS 87
    |||||

Qy 61 LFKDKKAMLFYYDQYQENNVDAQSGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNSTF 120
    |||||
Db 88 LFKDKKAMLFYYDQYQENNVDAQSGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNSTF 147
    |||||

Qy 121 TGFLLYHDTN 130
    |||||
Db 148 TGFLLYHDTN 157
    |||||

RESULT 8
US-10-659-782A-23
; Sequence 23, Application US/10659782A
; Publication No. US20050059015A1
; GENERAL INFORMATION:
; APPLICANT: Mintz, Liat
; TITLE OF INVENTION: Compositions, Reagents and Kits for and Methods of Diagnosing,
; FILE REFERENCE: 28238
; CURRENT APPLICATION NUMBER: US/10/659,782A
; CURRENT FILING DATE: 2003-09-11
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-659-782A-23

Query Match          100.0%; Score 708; DB 17; Length 160;
Best Local Similarity 100.0%; Pred. No. 5.7e-70;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FSVGLETVVTIPNMPIRFTKIFYNQONHYDSTGKFGHCNIPGLYFAVHITVYMKDVKS 60
    |||||
Db 31 FSVGLETVVTIPNMPIRFTKIFYNQONHYDSTGKFGHCNIPGLYFAVHITVYMKDVKS 90
    |||||

Qy 61 LFKDKKAMLFYYDQYQENNVDAQSGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNSTF 120
    |||||
Db 91 LFKDKKAMLFYYDQYQENNVDAQSGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNSTF 150
    |||||

Qy 121 TGFLLYHDTN 130
    |||||
Db 151 TGFLLYHDTN 160
    |||||

RESULT 9
US-10-325-717-10
; Sequence 10, Application US/10325717
; Publication No. US20030176328A1
; GENERAL INFORMATION:
; APPLICANT: Rasmussen, Poul Baad
; APPLICANT: Andersen, Kim Vilbourn
; APPLICANT: Pedersen, Anders Hjelholt
; APPLICANT: Schambye, Hans Thalesgaard
; APPLICANT: Halkier, Torben
; APPLICANT: Bogenes, Are
; TITLE OF INVENTION: Adiponectin Fragments and Conjugates
; FILE REFERENCE: 0251ue610
; CURRENT APPLICATION NUMBER: US/10/325,717
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/412,169
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US 60/394,117
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/375,492
; PRIOR FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US 60/343,482
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 163
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct Y111N-APM1 (82-244)
US-10-325-717-53

Query Match          100.0%; Score 708; DB 14; Length 163;
Best Local Similarity 100.0%; Pred. No. 5.8e-70;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FSVGLETVVTIPNMPIRFTKIFYNQONHYDSTGKFGHCNIPGLYFAVHITVYMKDVKS 60
    |||||
Db 34 FSVGLETVVTIPNMPIRFTKIFYNQONHYDSTGKFGHCNIPGLYFAVHITVYMKDVKS 93
    |||||

Qy 61 LFKDKKAMLFYYDQYQENNVDAQSGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNSTF 120
    |||||
Db 94 LFKDKKAMLFYYDQYQENNVDAQSGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNSTF 153
    |||||

Qy 121 TGFLLYHDTN 130
    |||||
Db 154 TGFLLYHDTN 163
    |||||

RESULT 10
US-10-325-717-53
; Sequence 53, Application US/10325717
; Publication No. US20030176328A1
; GENERAL INFORMATION:
; APPLICANT: Rasmussen, Poul Baad
; APPLICANT: Andersen, Kim Vilbourn
; APPLICANT: Pedersen, Anders Hjelholt
; APPLICANT: Schambye, Hans Thalesgaard
; APPLICANT: Halkier, Torben
; APPLICANT: Bogenes, Are
; TITLE OF INVENTION: Adiponectin Fragments and Conjugates
; FILE REFERENCE: 0251ue610
; CURRENT APPLICATION NUMBER: US/10/325,717
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/412,169
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US 60/394,117
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/375,492
; PRIOR FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US 60/343,482
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 163
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct Y111N-APM1 (82-244)
US-10-325-717-53

Query Match          100.0%; Score 708; DB 14; Length 163;
Best Local Similarity 100.0%; Pred. No. 5.8e-70;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FSVGLETVVTIPNMPIRFTKIFYNQONHYDSTGKFGHCNIPGLYFAVHITVYMKDVKS 60
    |||||
Db 34 FSVGLETVVTIPNMPIRFTKIFYNQONHYDSTGKFGHCNIPGLYFAVHITVYMKDVKS 93
    |||||

Qy 61 LFKDKKAMLFYYDQYQENNVDAQSGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNSTF 120
    |||||
Db 94 LFKDKKAMLFYYDQYQENNVDAQSGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNSTF 153
    |||||

Qy 121 TGFLLYHDTN 130
    |||||
Db 154 TGFLLYHDTN 163
    |||||
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; PRIOR APPLICATION NUMBER: US 60/375,492
; PRIOR FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US 60/343,482
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 163
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: apM1(82-244)
US-10-325-717-10

Query Match          100.0%; Score 708; DB 14; Length 163;
Best Local Similarity 100.0%; Pred. No. 5.8e-70;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FSVGLETVVTIPNMPIRFTKIFYNQONHYDSTGKFGHCNIPGLYFAVHITVYMKDVKS 60
    |||||
Db 34 FSVGLETVVTIPNMPIRFTKIFYNQONHYDSTGKFGHCNIPGLYFAVHITVYMKDVKS 93
    |||||

Qy 61 LFKDKKAMLFYYDQYQENNVDAQSGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNSTF 120
    |||||
Db 94 LFKDKKAMLFYYDQYQENNVDAQSGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNSTF 153
    |||||

Qy 121 TGFLLYHDTN 130
    |||||
Db 154 TGFLLYHDTN 163
    |||||

RESULT 10
US-10-325-717-53
; Sequence 53, Application US/10325717
; Publication No. US20030176328A1
; GENERAL INFORMATION:
; APPLICANT: Rasmussen, Poul Baad
; APPLICANT: Andersen, Kim Vilbourn
; APPLICANT: Pedersen, Anders Hjelholt
; APPLICANT: Schambye, Hans Thalesgaard
; APPLICANT: Halkier, Torben
; APPLICANT: Bogenes, Are
; TITLE OF INVENTION: Adiponectin Fragments and Conjugates
; FILE REFERENCE: 0251ue610
; CURRENT APPLICATION NUMBER: US/10/325,717
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/412,169
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US 60/394,117
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/375,492
; PRIOR FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US 60/343,482
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 163
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct Y111N-APM1 (82-244)
US-10-325-717-53

Query Match          100.0%; Score 708; DB 14; Length 163;
Best Local Similarity 100.0%; Pred. No. 5.8e-70;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FSVGLETVVTIPNMPIRFTKIFYNQONHYDSTGKFGHCNIPGLYFAVHITVYMKDVKS 60
    |||||
Db 34 FSVGLETVVTIPNMPIRFTKIFYNQONHYDSTGKFGHCNIPGLYFAVHITVYMKDVKS 93
    |||||

Qy 61 LFKDKKAMLFYYDQYQENNVDAQSGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNSTF 120
    |||||
Db 94 LFKDKKAMLFYYDQYQENNVDAQSGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNSTF 153
    |||||

Qy 121 TGFLLYHDTN 130
    |||||
Db 154 TGFLLYHDTN 163
    |||||
```

Db 94 LFKKDKAMLFYDQYQENNVDAQSGSVLLHLEVGDDQVWLQVYGEGERNGLYADNDNDSTF 153
QY 121 TGFLLYHDTN 130
Db 154 TGFLLYHDTN 163

RESULT 11

US-10-325-717-13
; Sequence 13, Application US/10325717
; Publication No. US20030176328A1
; GENERAL INFORMATION:
; APPLICANT: Rasmussen, Poul Baad
; APPLICANT: Andersen, Kim Vilbourn
; APPLICANT: Pedersen, Anders Hjelholt
; APPLICANT: Schambye, Hans Thalsgaard
; APPLICANT: Halkier, Torben
; APPLICANT: Bogenes, Are
; TITLE OF INVENTION: Adiponectin Fragments and Conjugates
; FILE REFERENCE: 0251us610
; CURRENT APPLICATION NUMBER: US/10/325,717
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/412,169
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US 60/394,117
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/375,492
; PRIOR FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US 60/343,482
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 187
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: apM1(58-244)
US-10-325-717-13

Query Match 100.0%; Score 708; DB 14; Length 187;
Best Local Similarity 100.0%; Pred. No. 6.9e-70;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FSVGLETTYTIPMPPIRFTKIFYNQNNHYDGSFGKFCNCIPGLYFAVHITVYMKDVKS 60
Db 58 FSVGLETTYTIPMPPIRFTKIFYNQNNHYDGSFGKFCNCIPGLYFAVHITVYMKDVKS 117
QY 61 LFKKDKAMLFYDQYQENNVDAQSGSVLLHLEVGDDQVWLQVYGEGERNGLYADNDNDSTF 120
Db 118 LFKKDKAMLFYDQYQENNVDAQSGSVLLHLEVGDDQVWLQVYGEGERNGLYADNDNDSTF 177
QY 121 TGFLLYHDTN 130
Db 178 TGFLLYHDTN 187

RESULT 12

US-10-325-717-12
; Sequence 12, Application US/10325717
; Publication No. US20030176328A1
; GENERAL INFORMATION:
; APPLICANT: Rasmussen, Poul Baad
; APPLICANT: Andersen, Kim Vilbourn
; APPLICANT: Pedersen, Anders Hjelholt
; APPLICANT: Schambye, Hans Thalsgaard
; APPLICANT: Halkier, Torben
; APPLICANT: Bogenes, Are
; TITLE OF INVENTION: Adiponectin Fragments and Conjugates
; FILE REFERENCE: 0251us610
; CURRENT APPLICATION NUMBER: US/10/325,717
; CURRENT FILING DATE: 2002-12-20

; PRIOR APPLICATION NUMBER: US 60/412,169
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US 60/394,117
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/375,492
; PRIOR FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US 60/343,482
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: apM1(52-244)
US-10-325-717-12

Query Match 100.0%; Score 708; DB 14; Length 193;
Best Local Similarity 100.0%; Pred. No. 7.2e-70;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FSVGLETTYTIPMPPIRFTKIFYNQNNHYDGSFGKFCNCIPGLYFAVHITVYMKDVKS 60
Db 64 FSVGLETTYTIPMPPIRFTKIFYNQNNHYDGSFGKFCNCIPGLYFAVHITVYMKDVKS 123
QY 61 LFKKDKAMLFYDQYQENNVDAQSGSVLLHLEVGDDQVWLQVYGEGERNGLYADNDNDSTF 120
Db 124 LFKKDKAMLFYDQYQENNVDAQSGSVLLHLEVGDDQVWLQVYGEGERNGLYADNDNDSTF 183
QY 121 TGFLLYHDTN 130
Db 184 TGFLLYHDTN 193

RESULT 13

US-10-325-717-3
; Sequence 3, Application US/10325717
; Publication No. US20030176328A1
; GENERAL INFORMATION:
; APPLICANT: Rasmussen, Poul Baad
; APPLICANT: Andersen, Kim Vilbourn
; APPLICANT: Pedersen, Anders Hjelholt
; APPLICANT: Schambye, Hans Thalsgaard
; APPLICANT: Halkier, Torben
; APPLICANT: Bogenes, Are
; TITLE OF INVENTION: Adiponectin Fragments and Conjugates
; FILE REFERENCE: 0251us610
; CURRENT APPLICATION NUMBER: US/10/325,717
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/412,169
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US 60/394,117
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/375,492
; PRIOR FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US 60/343,482
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 203
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: apM1(42-244)
US-10-325-717-3

Query Match 100.0%; Score 708; DB 14; Length 203;
Best Local Similarity 100.0%; Pred. No. 7.6e-70;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FSVGLETTYTIPMPPIRFTKIFYNQNNHYDGSFGKFCNCIPGLYFAVHITVYMKDVKS 60

Db 74 FSVGLETVVTIPNMPIRFTKIFYNQNNHYDSTGKFKHNPGLYFAVHITVYMKDVKVS 133
QY 61 LFKKDKAMLFTYDQYQENNVDAAGSVLLHLEVGQVWLQVYGEGERNGLYADNDNDSTF 120
Db 134 LFKKDKAMLFTYDQYQENNVDAAGSVLLHLEVGQVWLQVYGEGERNGLYADNDNDSTF 193
QY 121 TGFLLYHDTN 130
Db 194 TGFLLYHDTN 203

RESULT 14

US-10-325-717-2
; Sequence 2, Application US/10325717
; Publication No. US20030176328A1
; GENERAL INFORMATION:
; APPLICANT: Rasmussen, Poul Baad
; APPLICANT: Andersen, Kim Vilbourn
; APPLICANT: Pedersen, Anders Hjelholt
; APPLICANT: Schambye, Hans Thalsgaard
; APPLICANT: Halkier, Torben
; APPLICANT: Bogenes, Aye
; TITLE OF INVENTION: Adiponectin Fragments and Conjugates
; FILE REFERENCE: 0251us610
; CURRENT APPLICATION NUMBER: US/10/325,717
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/412,169
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US 60/394,117
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/375,492
; PRIOR FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US 60/343,482
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: apm1(19-244)
US-10-325-717-2

Query Match 100.0%; Score 708; DB 14; Length 226;
Best Local Similarity 100.0%; Pred. No. 8.7e-70;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSVGLETVVTIPNMPIRFTKIFYNQNNHYDSTGKFKHNPGLYFAVHITVYMKDVKVS 60
Db 97 FSVGLETVVTIPNMPIRFTKIFYNQNNHYDSTGKFKHNPGLYFAVHITVYMKDVKVS 156
QY 61 LFKKDKAMLFTYDQYQENNVDAAGSVLLHLEVGQVWLQVYGEGERNGLYADNDNDSTF 120
Db 157 LFKKDKAMLFTYDQYQENNVDAAGSVLLHLEVGQVWLQVYGEGERNGLYADNDNDSTF 216
QY 121 TGFLLYHDTN 130
Db 217 TGFLLYHDTN 226

RESULT 15

US-10-189-493-2
; Sequence 2, Application US/10189493
; Publication No. US20030166551A1
; GENERAL INFORMATION:
; APPLICANT: Otsuka Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: Smooth muscle growth inhibitory composition, a
; TITLE OF INVENTION: diagnostic method for arteriosclerosis and a kit
; FILE REFERENCE: P98-51
; CURRENT APPLICATION NUMBER: US/10/189,493

; CURRENT FILING DATE: 2002-07-08
; PRIOR APPLICATION NUMBER: US/09/530,423
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Abdominal fat tissue from myoma uteri
US-10-189-493-2

Query Match 100.0%; Score 708; DB 14; Length 231;
Best Local Similarity 100.0%; Pred. No. 9e-70;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSVGLETVVTIPNMPIRFTKIFYNQNNHYDSTGKFKHNPGLYFAVHITVYMKDVKVS 60
Db 102 FSVGLETVVTIPNMPIRFTKIFYNQNNHYDSTGKFKHNPGLYFAVHITVYMKDVKVS 161
QY 61 LFKKDKAMLFTYDQYQENNVDAAGSVLLHLEVGQVWLQVYGEGERNGLYADNDNDSTF 120
Db 162 LFKKDKAMLFTYDQYQENNVDAAGSVLLHLEVGQVWLQVYGEGERNGLYADNDNDSTF 221
QY 121 TGFLLYHDTN 130
Db 222 TGFLLYHDTN 231

Search completed: May 8, 2005, 15:47:33
Job time : 56.967 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 6, 2005, 17:08:11 ; Search time 14.1497 Seconds

(Without alignments)
883.992 Million cell updates/sec

Title: US-10-072-159-11

Perfect score: 708

Sequence: 1 FSVGLETTYVTIPNMPIRFTK.....YADNDSTFGFLVHDTN 130

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
1	708	100.0	244	2 UC4708	gelatin-binding 28
2	297.5	42.0	674	2 S23297	collagen alpha 1(X
3	287.5	40.6	680	1 CGH01D	collagen alpha 1(X
4	280.5	39.6	674	2 S13301	collagen alpha 1(X
5	280.5	39.6	680	2 S31216	collagen alpha 1(X
6	273.5	38.6	743	1 S23779	collagen alpha 1(X
7	270.5	38.2	744	2 S15435	collagen alpha 1(X
8	267.5	37.8	744	1 A34446	collagen alpha 1(X
9	263.5	37.2	744	1 S23298	collagen alpha 1(X
10	258.5	36.5	170	2 B57131	collagen alpha 2(X
11	258.5	36.5	635	2 A57131	collagen alpha 2(X
12	243.5	34.4	219	2 T14782	hypothetical prote
13	239	30.9	245	1 C1H0C	complement subcomp
14	219	30.9	423	2 A5797	collagen precursor
15	208.5	29.4	246	2 S29328	complement subcomp
16	186	26.3	253	2 I49560	complement protein
17	184	26.0	253	2 I49560	complement C1q B c
18	182.5	25.8	253	1 C1H0B	complement subcomp
19	178	25.1	215	2 B48150	hibernation-relate
20	176	24.9	136	2 A48150	hibernation-relate
21	174	24.6	215	2 C48150	hibernation-relate
22	156	22.0	245	2 S19018	complement subcomp
23	151.5	21.4	245	1 C1H0A	complement subcomp
24	119.5	16.9	224	2 A60032	cerebellin-like gl
25	116.5	16.5	193	2 A37873	cerebellin precurs
26	113.5	16.0	1228	2 A57384	multimerin, endoth
27	86.5	12.2	213	2 B81360	probable protein d
28	82	11.6	280	1 G70126	phosphate ABC tran
29	77	10.9	687	2 E69733	PSX prophage ORF

30	76	10.7	463	2 A38463	fibrinogen beta ch
31	76	10.7	1032	2 A11697	alpha-mannosidase
32	75.5	10.7	527	2 T27572	hypothetical prote
33	74.5	10.5	1048	2 H64459	hypothetical prote
34	74	10.5	450	2 S57837	lymphoid-specific
35	74	10.5	992	2 T08772	hypothetical prote
36	74	10.5	1036	2 AG1326	alpha-mannosidase
37	73.5	10.4	1963	2 B98002	IgA-specific metal
38	73	10.3	366	2 B69949	phage-related prot
39	72.5	10.2	377	2 B57745	transcription fact
40	72	10.2	532	2 JC1392	monophenol monooxy
41	72	10.2	1797	2 F69195	cell surface glyco
42	71.5	10.1	183	2 A53516	ubiquitin-protein
43	71.5	10.1	183	2 JC4308	ubiquitin-protein
44	71.5	10.1	288	2 T33224	hypothetical prote
45	71.5	10.1	556	2 T03114	segment protein -

ALIGNMENTS

RESULT 1

UC4708

gelatin-binding 28X protein precursor - human

C:Species: Homo sapiens (man)

C>Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004

C/Accession: UC4708, UC4944

R/Maeda, K.; Okubo, K.; Shimomura, I.; Funahashi, T.; Matsuzawa, Y.; Matsubara, K.

Biochem. Biophys. Res. Commun. 221, 286-289, 1996

A>Title: cDNA cloning and expression of a novel adipose specific collagen-like factor,

A/Reference number: UC4708, MUID:96224171, PMID:8619847

A/Accession: UC4708

A/Molecule type: mRNA

A/Residues: 1-244 <MAE>

A/Cross-references: UNIPROT:Q15848; DDBJ:D45371; NID:9871886; PID:BAA08227.1; PID:9871

A/Experimental source: adipose tissue

R/Makino, Y.; Tobe, T.; Choi-Mura, N.H.; Maeda, T.; Tomita, M.

U. Biochem. 120, 803-812, 1996

F:114-241/Domain: complement C1q carboxy1-terminal homology <C1Q>

F:230/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

Best Local Similarity 100.0%; Score 708; DB 2; Length 244;

Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSVGLETTYVTIPNMPIRFTKIFPNQNNHDSGKGFHCNIPGLYFAVHTTVMKQVKS 60

DB 115 FSVGLETTYVTIPNMPIRFTKIFPNQNNHDSGKGFHCNIPGLYFAVHTTVMKQVKS 174

QY 61 LFKKDRAMLFYDQYQENNVDAAGSVLLHLEVGQVWLQVYGEGRNGLYADNDSTF 120

DB 175 LFKKDRAMLFYDQYQENNVDAAGSVLLHLEVGQVWLQVYGEGRNGLYADNDSTF 234

QY 121 TGFLLVHDTN 130

DB 235 TGFLLVHDTN 244

RESULT 2

S23297
N:Alternate names: type X collagen
C:Species: Gallus gallus (chicken)
C:Date: 07-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S23297; A31896; S65594; S77711; I50218
R:Ninomiya, Y.; Castanola, P.; Gerecke, D.; Gordon, M.K.; Jacenko, O.; LuValle, P.; McC
magnuchi, N.; Olsen, B.R.
in Extracellular Matrix Genes, Sandell L.J. and Boyd C.D., eds., pp.79-114, Academic Pre
A:Title: The molecular biology of collagens with short triple-helical domains.
A:Reference number: S22243
A:Accession: S23297
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-674 <NIN>
A:Cross-references: UNIPROT:P08125
R:LuValle, P.; Ninomiya, Y.; Rosenblum, N.D.; Olsen, B.R.
J. Biol. Chem. 263, 18378-18385, 1988
A:Title: The type X collagen gene. Intron sequences split the 5'-untranslated region and
A:Reference number: A31896; MUID:89054019; PMID:2461368
A:Accession: A31896
A:Molecule type: mRNA
A:Residues: 1-75 <LUV>
R:Ninomiya, Y.; Gordon, M.; van der Rest, M.; Schmid, T.; Linsemaier, T.; Olsen, B.R.
J. Biol. Chem. 261, 5041-5050, 1986
A:Title: The developmentally regulated type X collagen gene contains a long open reading
A:Reference number: I50218; MUID:86168227; PMID:3082876
A:Accession: S65594
A:Molecule type: DNA
A:Residues: 'T','9','D','11-12','EDQMKLYLFMTM','30-31','TCKSGRAFTYTMILQNMADLVSSHT','48-89','L',
629,'PQAVLSISRTICSGSCQIONPMVSIPLNMFILSOVSYLKSNINPLTMS' <NINI>
A:Cross-references: EMBL:M13496; NID:g211659; PIDN:AAA48736.1; PID:g211700
A:Accession: S77711
A:Molecule type: protein
A:Residues: 104-112, 'X', 114-117, 453-466 <NIN2>
C:Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology
C:Keywords: coiled coil; extracellular matrix; glycoprotein; homotrimer; hydroxyproline;
F:1-18/Domain: signal sequence #status predicted <SIG>
F:547-673/Domain: complement C1q carboxyl-terminal homology <CIQ>
F:453-456/Modified site: hydroxyproline (Pro) #status experimental
F:611/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 42.0%; Score 297.5; DB 2; Length 674;
Best Local Similarity 47.6%; Pred. No. 6-8e-22;
Matches 59; Conservative 21; Mismatches 43; Indels 1; Gaps 1;

Oy 1 FSVGLIETVTLPMPIRFTKTFYNOQNHDSGTFKPHCNIPGLYFPAHYITVMKDVYS 60
Db 548 FTVLSKAVPGATVPIKFDKILYNRQOHYDPRGTGIFTCRIPGLYFSPVHAKGTNWWVA 607
Oy 61 LFKDKALFTYDOQENNVNQAAGSVLLHLEVGQWMLQVYGBERNGLYADNDNSTF 120
Db 608 LYKNSPVMYTYDEYQGYLDQAGSAVIDLMENDQWLDL--PNSSENGLYSSEYVHSEF 666
Oy 121 TGFL 124
Db 667 SGFL 670

RESULT 3
CGHUID
collagen alpha 1(X) chain precursor - human
N:Alternate names: procollagen alpha 1(X) chain
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C:Accession: S26396; S30086; S18286; S18249; A43901; I51870; S21856
R:Reichenberger, E.; Beier, F.; LuValle, P.; Olsen, B.R.; von der Mark, K.; Bertling, W.
FEBS Lett. 311, 305-310, 1992
A:Title: Genomic organization and full-length cDNA sequence of human collagen X.
A:Reference number: S26396; MUID:93012005; PMID:1397333
A:Accession: S26396
A:Molecule type: DNA
A:Residues: 1-680 <REI>

A:Cross-references: UNIPROT:Q03692; EMBL:X68952; EMBL:X72578; EMBL:X72579; EMBL:X72580; R:Apfe, S.S.
submitted to the EMBL Data Library, March 1992
A:Reference number: S30085
A:Accession: S30086
A:Molecule type: DNA
A:Residues: 'TTPFGWCMVCCL', 52-680 <APT>
A:Cross-references: EMBL:X65120; NID:g23129
A>Note: the initial difference is probably due to translation of an intronic sequence
R:Apfe, S.; Matzel, M.G.; Olsen, B.R.
FEBS Lett. 282, 393-396, 1991
A:Title: Cloning of human alpha-1(X) collagen DNA and localization of the COL10A1 gene t
A:Reference number: S15826; MUID:91243838; PMID:2037056
A:Accession: S15826
A:Molecule type: DNA
A:Residues: 561-647, 'G', 649-666 <AP2>
A:Cross-references: EMBL:X58879; NID:g30013; PIDN:CAA41686.1; PID:g30014
R:Thomas, J.T.; Cresswell, C.J.; Rash, B.; Nicolai, H.; Jones, T.; Solomon, E.; Grant, M
Blochem. J. 280, 617-623, 1991
A:Title: The human collagen X gene. Complete primary translated sequence and chromosomal
A:Reference number: S18249; MUID:92109659; PMID:1764025
A:Accession: S18249
A:Molecule type: DNA
A:Residues: 1-26, 'T', 28-680 <THO>
A:Cross-references: EMBL:X60382; NID:g30094; PIDN:CAA42933.1; PID:g30095
A>Note: the sequence from Fig. 3 is inconsistent with that from Fig. 2 in having 532-Ala
R:Reichenberger, E.; Aigner, T.; von der Mark, K.; Stoss, H.; Bertling, W.
Dev. Biol. 148, 562-572, 1991
A:Title: In situ hybridization studies on the expression of type X collagen in fetal hum
A:Reference number: A43901; MUID:92077285; PMID:1743401
A:Accession: A43901
A:Molecule type: mRNA
A:Residues: 547-656 <RE2>
A:Cross-references: GB:D57494; NID:g339884; PIDN:AAA61221.1; PID:g553796
A>Note: sequence extracted from NCBI backbone (NCBI:69012, NCBI:69014)
R:Wallis, G.A.; Rash, B.; Sweetman, W.A.; Thomas, J.T.; Super, M.; Evans, G.; Grant, M.B
Am. J. Hum. Genet. 54, 169-178, 1994
A:Title: Amino acid substitutions of conserved residues in the carboxyl-terminal domain
pe Schmid.
A:Reference number: I51870; MUID:94136476; PMID:8304336
A:Accession: I51870
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 520-597, 'D', 599-680 <WAL>
A:Cross-references: GB:S68531; NID:g545180; PIDN:AA60615.1; PID:g545181
A>Note: mutant sequence from patient with metaphase chondrodysplasia type Schmid
C:Comment: Proline and lysines at the third position of the tripeptide repeating unit (e
ed and subsequently O-glycosylated.
C:Genetics:
A:Gene: GDB:COL10A1
A:Cross-references: GDB:128635; OMIM:120110
A:Map position: 6q21-6q22
A:Introns: 52/1
A>Note: a defect in this gene may cause Schmid metaphyseal chondrodysplasia
C:Complex: type X collagen may be a homotrimer
C:Function:
A:Description: structural component of extracellular fibrous polymer specifically and tr
be important for skeletogenesis
C:Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology
C:Keywords: coiled coil; extracellular matrix; glycoprotein; homotrimer; hydroxyllysine;
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-680/Product: collagen alpha 1(X) chain #status predicted <MAT>
F:19-56/Domain: amino-terminal nonhelical #status predicted <NC2>
F:57-519/Region: interrupted helical
F:520-680/Domain: amino-terminal nonhelical #status predicted <NC1>
F:553-679/Domain: complement C1q carboxyl-terminal homology <CIQ>
F:617/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 40.6%; Score 287.5; DB 1; Length 680;
Best Local Similarity 46.4%; Pred. No. 6-9e-21;
Matches 58; Conservative 19; Mismatches 47; Indels 1; Gaps 1;

QY 1 FSVGLETTYITPMPPIRFTKIFYNQONHVDGSGTKFHCNIPGLYFAVHITVMKDVKS 60
 DB 554 FTVILSKAVPAIGTPIPFKILYNROQHDPKRGIFTCQIPGIYFSYHNVHVGTHWVG 613
 QY 61 LFKKDKAMLFYDQYQENNVDAQSGSVLLHLLEVGDQVWLQVYGEGRNGLYADNDSDTF 120
 DB 614 LYKNGTPWVYTYDEYTKGYLDQASGSAIIDLITENDQVWLQ-LPNAESNGLYSEYVHSSF 672
 QY 121 TGFLL 125
 DB 673 SGFLV 677

RESULT 4

S31301
 collagen alpha 1(X) chain precursor - bovine
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 21-Nov-1993 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004
 C:Accession: S13301
 R:Thomas, J.T.; Kwan, A.P.L.; Grant, M.E.; Boot-Handford, R.P.
 Biochem. J. 273, 141-148, 1991
 A>Title: Isolation of cDNAs encoding the complete sequence of bovine type X collagen. EV
 A:Reference number: S13301; MUID:91113131; PMID:1703407
 A:Accession: S13301
 A:Molecule type: mRNA
 A:Residues: 1-674 <THO>
 A:Cross-references: UNIPROT:P23206; EMBL:X53556; NID:g263; PIDN:CA437624.1; PID:g264
 C:Genetic8:
 A:Gene: COL10A1
 C:Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology
 C:Keywords: coiled coil; extracellular matrix; glycoprotein; homotrimer
 F:1-18/Domain: signal sequence #status predicted <Sig>
 F:19-674/Product: collagen alpha 1(X) chain #status predicted <MAT>
 F:547-673/Domain: complement C1q carboxyl-terminal homology <ClQ>

Query Match 39.6%; Score 280.5; DB 2; Length 674;
 Best Local Similarity 46.4%; Pred. No. 3.5e-20;
 Matches 58; Conservative 18; Mismatches 48; Indels 1; Gaps 1;

QY 1 FSVGLETTYITPMPPIRFTKIFYNQONHVDGSGTKFHCNIPGLYFAVHITVMKDVKS 60
 DB 548 FTVILSKAVPAIGTPIPFKILYNROQHDPKRGIFTCQIPGIYFSYHNVHVGTHWVG 607
 QY 61 LFKKDKAMLFYDQYQENNVDAQSGSVLLHLLEVGDQVWLQVYGEGRNGLYADNDSDTF 120
 DB 608 LYKNGTPWVYTYDEYTKGYLDQASGSAIIDLITENDQVWLQ-LPNAESNGLYSEYVHSSF 666
 QY 121 TGFLL 125
 DB 667 SGFLV 671

RESULT 5

S31216
 collagen alpha 1(X) chain precursor - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
 C:Accession: S31216; S28807; S22215; S30127; I48299; S26397; S31830
 R:Kong, R.Y.C.; Kwan, K.M.; Lau, E.T.; Thomas, J.T.; Boot-Handford, R.P.; Grant, M.E.; C
 Eur. J. Biochem. 213, 99-111, 1993
 A>Title: Intron-exon structure, alternative use of promoter and expression of the mouse
 A:Reference number: S31216; MUID:93238750; PMID:8477738
 A:Accession: S31216
 A:Molecule type: DNA
 A:Residues: 1-680 <KON>
 A:Cross-references: UNIPROT:Q05306; EMBL:Z21610; NID:949793; PIDN:CAA79736.1; PID:g49794
 R:Elima, K.; Berola, I.; Rosati, R.; Metsaeranta, M.; Garofalo, S.; Peraelae, M.; de Cro
 Biochem. J. 289, 247-253, 1993
 A>Title: The mouse collagen X gene: complete nucleotide sequence, exon structure and exp
 A:Reference number: S28807; MUID:93143676; PMID:8424763
 A:Accession: S28807
 A:Molecule type: DNA
 A:Residues: 1-285, 'A', 287-680 <ELI>

A:Cross-references: EMBL:X67348; NID:950480; PIDN:CAA7763.1; PID:g50481
 R:Elima, K.; Metsaeranta, M.; Kallio, J.; Peraelae, M.; Berola, I.; Garofalo, S.; de Cr
 Biochim. Biophys. Acta 1120, 78-80, 1992
 A>Title: Specific hybridization probes for mouse alpha-2(I)X and alpha-1(X) collagen mR
 A:Reference number: S22215; MUID:92182017; PMID:1543751
 A:Accession: S22215
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 385-450, 'K', 452-627 <ELA>
 A:Cross-references: EMBL:X63013; NID:g49795; PIDN:CAA44741.1; PID:g49796
 R:Appte, S.S.; Olsen, B.R.
 Matrix 13, 165-179, 1993
 A>Title: Characterization of the mouse type X collagen gene.
 A:Reference number: S30127; MUID:93261348; PMID:8492743
 A:Accession: S30127
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-12, 'F', 14-26, 'S', 28-247, 'L', 249-285, 'A', 287-305, 'F', 307-416, 'S', 418-499, 'I
 R:Appte, S.S.; Seidlin, M.F.; Hayashi, M.; Olsen, B.R.
 Eur. J. Biochem. 206, 217-224, 1992
 A>Title: Cloning of the human and mouse type X collagen genes and mapping of the mouse
 A:Reference number: I48299; MUID:92267014; PMID:1587271
 A:Accession: I48299
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 52-247, 'L', 249-285, 'A', 287-305, 'F', 307-416, 'S', 418-499, 'L', 501-566, 'C', 568, 'I
 A:Cross-references: EMBL:X65121; NID:g50482; PIDN:CAA46237.1; PID:g667031
 R:Summers, T.A.; Irwin, W.H.; Wayne, R.; Ballan, G.
 J. Biol. Chem. 263, 581-587, 1988
 A>Title: Monoclonal antibodies to type X collagen. Biosynthetic studies using an antibo
 A:Reference number: S26397; MUID:88087150; PMID:2826450
 A:Accession: S26397
 A:Molecule type: protein
 A:Residues: 'SDGTFSD', 24-26, 'KQ' <SUM>
 C:Genetics:
 A:Gene: Col10a-1
 A:Map position: 10
 A:Introns: 51/3

C:Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology
 C:Keywords: coiled coil; extracellular matrix; glycoprotein; homotrimer
 F:1-18/Domain: signal sequence #status predicted <Sig>
 F:19-680/Product: collagen alpha 1(X) chain #status predicted <MAT>
 F:553-679/Domain: complement C1q carboxyl-terminal homology <ClQ>

Query Match 39.6%; Score 280.5; DB 2; Length 680;
 Best Local Similarity 44.8%; Pred. No. 3.5e-20;
 Matches 56; Conservative 20; Mismatches 48; Indels 1; Gaps 1;

QY 1 FSVGLETTYITPMPPIRFTKIFYNQONHVDGSGTKFHCNIPGLYFAVHITVMKDVKS 60
 DB 554 FTVILSKAVPAIGTPIPFKILYNROQHDPKRGIFTCQIPGIYFSYHNVHVGTHWVG 613
 QY 61 LFKKDKAMLFYDQYQENNVDAQSGSVLLHLLEVGDQVWLQVYGEGRNGLYADNDSDTF 120
 DB 614 LYKNGTPWVYTYDEYTKGYLDQASGSAIIDLITENDQVWLQ-LPNAESNGLYSEYVHSSF 672
 QY 121 TGFLL 125
 DB 673 SGFLV 677

RESULT 6

S23779
 collagen alpha 1(VIII) chain - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C:Accession: S23779
 R:Murgachi, Y.; Shiota, C.; Inoue, M.; Ooshima, A.; Olsen, B.R.; Ninomiya, Y.
 Eur. J. Biochem. 207, 895-902, 1992
 A>Title: Alpha-1(VIII)-collagen gene transcripts encode a short-chain collagen polypept
 A:Reference number: S23779; MUID:92362626; PMID:1499564
 A:Accession: S23779
 A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-743 <MUR>
A:Cross-references: UNIPROT:Q00780; EMBL:X66976; NID:g50493; PIDN:CAA47387.1; PID:g13599
C:Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology
F:616-742/Domain: complement C1q carboxyl-terminal homology <C1Q>
Query Match 38.6%; Score 273.5; DB 1; Length 743;
Best Local Similarity 45.1%; Pred. No. 2e-19;
Matches 55; Conservative 27; Mismatches 35; Indels 5; Gaps 2;
Qy 9 VTIP---NMPRTKIFVYNOQNHVDSGTGFHCNIPGLYFAVHIITVMKDVKSLFKK 64
Db 621 LTVPEPPVGAIVKPKDKLYNGRQYNPQTGIFTCEVPGVYFAVHCKGQVWVWALFKN 680
Qy 65 DKAMFTVDOYQENNVDQAGSVLLHLEVDQVWLQVYGEGERNGLYADNDNSTFTGFLY 124
Db 681 NEPMWYTYDEYKKGFLDQAGSAVLLLRPGDVRFLQNPSE-QAAGLYAGQYVHSSFSGLY 739
Qy 125 LY 126
Db 740 LY 741
RESULT 7
S15435
collagen alpha 1(VIII) chain precursor - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
A:Accession: S15435
R:Muragaki, Y.; Mattei, M.G.; Yamaguchi, N.; Olsen, B.R.; Nimomiya, Y.
Eur. J. Biochem. 197, 615-622, 1991
A:Title: The complete primary structure of the human alpha-1(VIII) chain and assignment
A:Reference number: S15435; MUID:91231001; PMID:2029894
A:Accession: S15435
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-744 <MUR>
A:Cross-references: UNIPROT:P27658; EMBL:X57527; NID:g30081; PIDN:CAA40748.1; PID:g30082
C:Genetics:
A:Gene: GDB:COL8A1
A:Cross-references: GDB:128104; OMIM:120251
A:Map position: 3q11.1-3q13.2
C:Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-744/Product: collagen alpha 1(VIII) chain #status predicted <MAT>
F:21-117/Region: amino-terminal nonhelical
F:118-571/Region: interrupted helical
F:572-744/Region: carboxyl-terminal nonhelical
F:617-743/Domain: complement C1q carboxyl-terminal homology <C1Q>
Query Match 38.2%; Score 270.5; DB 2; Length 744;
Best Local Similarity 45.5%; Pred. No. 3.9e-19;
Matches 51; Conservative 28; Mismatches 34; Indels 1; Gaps 1;
Qy 15 PIRFTKIFVYNOQNHVDSGTGFHCNIPGLYFAVHIITVMKDVKSLFKKAMFTYDQ 74
Db 632 PVRNKKLLYNRQYNPQTGIFTCEVPGVYFAVHCKGQVWVWALFKNNEPVWYTYDE 691
Qy 75 YQENNVDQAGSVLLHLEVDQVWLQVYGEGERNGLYADNDNSTFTGFLY 126
Db 692 YKKGFLDQAGSAVLLLRPGDVRFLQNPSE-QAAGLYAGQYVHSSFSGLY 742
RESULT 8
A34246
collagen alpha 1(VIII) chain precursor - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
A:Accession: A34246
R:Yamaguchi, N.; Benya, P.D.; van der Rest, M.; Nimomiya, Y.
J. Biol. Chem. 264, 16022-16029, 1989
A:Title: The cloning and sequencing of alpha 1(VIII) collagen cDNAs demonstrate that type
omains similar to those of type X collagen.

A:Reference number: A34246; MUID:89380199; PMID:2476437
A:Accession: A34246
A:Molecule type: mRNA
A:Residues: 1-744 <YAM>
A:Cross-references: UNIPROT:P14282; GB:J05042; NID:g164895; PIDN:AAA31204.1; PID:g164896
C:Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-744/Product: collagen alpha 1(VIII) chain #status predicted <MAT>
F:21-117/Region: amino-terminal nonhelical
F:118-571/Region: interrupted helical
F:572-744/Region: carboxyl-terminal nonhelical
F:617-743/Domain: complement C1q carboxyl-terminal homology <C1Q>
Query Match 37.8%; Score 267.5; DB 1; Length 744;
Best Local Similarity 45.5%; Pred. No. 7.9e-19;
Matches 51; Conservative 28; Mismatches 32; Indels 1; Gaps 1;
Qy 15 PIRFTKIFVYNOQNHVDSGTGFHCNIPGLYFAVHIITVMKDVKSLFKKAMFTYDQ 74
Db 632 PIKFDRLLYNRQYNPQTGIFTCEVPGVYFAVHCKGQVWVWALFKNNEPVWYTYDE 691
Qy 75 YQENNVDQAGSVLLHLEVDQVWLQVYGEGERNGLYADNDNSTFTGFLY 126
Db 692 YKKGFLDQAGSAVLLLRPGDVRFLQNPSE-QAAGLYAGQYVHSSFSGLY 742
RESULT 9
S23298
collagen alpha 1(VIII) chain - chicken
C:Species: Gallus gallus (chicken)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
A:Accession: S23298
R:Nimomiya, Y.; Castagnola, P.; Gerecke, D.; Gordon, M.K.; Jacenko, O.; LuValle, P.; McC
maguchi, N.; Olsen, B.R.
in Extracellular Matrix Genes, Sandell L.V. and Boyd C.D., eds., pp 79-114, Academic Pre
A:Title: The molecular biology of collagens with short triple-helical domains.
A:Reference number: S22243
A:Accession: S23298
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-744 <NIN>
A:Cross-references: UNIPROT:Q7LZR2
C:Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology
F:617-743/Domain: complement C1q carboxyl-terminal homology <C1Q>
Query Match 37.2%; Score 263.5; DB 1; Length 744;
Best Local Similarity 45.5%; Pred. No. 2e-18;
Matches 51; Conservative 27; Mismatches 33; Indels 1; Gaps 1;
Qy 15 PIRFTKIFVYNOQNHVDSGTGFHCNIPGLYFAVHIITVMKDVKSLFKKAMFTYDQ 74
Db 632 PIKFDRLLYNRQYNPQTGIFTCEVPGVYFAVHCKGQVWVWALFKNNEPVWYTYDE 691
Qy 75 YQENNVDQAGSVLLHLEVDQVWLQVYGEGERNGLYADNDNSTFTGFLY 126
Db 692 YKKGFLDQAGSAVLLLRPGDVRFLQNPSE-QAAGLYAGQYVHSSFSGLY 742
RESULT 10
B57131
collagen alpha 2(VIII) chain - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 03-Nov-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
A:Accession: B57131
R:Muragaki, Y.; Jacenko, O.; Apte, S.; Mattei, M.G.; Nimomiya, Y.; Olsen, B.R.
J. Biol. Chem. 266, 7721-7727, 1991
A:Title: The alpha2(VIII) collagen gene. A novel member of the short chain collagen fami
A:Reference number: A57131; MUID:91210292; PMID:2019595
A:Accession: B57131
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-170 <MUR>
A:Cross-references: UNIPROT:P25318; GB:M60833

C:Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology
F:43-169/Domain: complement C1q carboxyl-terminal homology <C1Q>

Query Match 36.5%; Score 258.5; DB 2; Length 170;
Best Local Similarity 40.8%; Pred. No. 1.1e-18;

Matches 51; Conservative 27; Mismatches 46; Indels 1; Gaps 1;

QY 1 FSVGLTETVYTIIPMPPIRFTKIFYNQONHVDSTGKFKHCNIPGLYFPAHYHTVYMKDVKYS 60

DB 44 FTAVLTSPPASGMPVRFRTLLNGHSGNVPATGISCPVGSVYFPAHYHVKGTWVA 103

QY 61 LFKKDKAMLETTYDOYQENNVDAQSGSVLLHLLEVGDQVWLQVYGEGERNGLYADNDSTF 120

DB 104 LYKNNVPATYTYDEYKKGVLDDQASGAVQLRPNDDVWVQIPSD-QANGLYSTREYIHSSP 162

QY 121 TGFLL 125

DB 163 SGFL 167

RESULT 11

collagen alpha 2(VIII) chain - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 03-Nov-1995 #sequence_rev1sion 03-Nov-1995 #text_change 09-Jul-2004

C:Accession: A57131

A:Title: The alpha2(VIII) collagen gene. A novel member of the short chain collagen faml

A:Reference number: A57131, PMID:91210292; PMID:2019595

A:Accession: A57131

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-635 <MUR>

A:Cross-references: UNIPROT:P25067; GB:M60832; NID:g171718; PIDN:AAA62822.1; PID:g171719

A:Gene: COL8A2

A:Cross-references: GDB:127812; OMIM:120252

C:Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology

F:1-11/Domain: amino-terminal nonhelical (fragment) #status predicted <NC2>

F:12-468/Region: interrupted helical

F:469-635/Domain: carboxyl-terminal nonhelical #status predicted <NC7>

F:508-634/Domain: complement C1q carboxyl-terminal homology <C1Q>

Query Match

Best Local Similarity 36.5%; Score 258.5; DB 2; Length 635;

Matches 50; Conservative 29; Mismatches 45; Indels 1; Gaps 1;

QY 1 FSVGLTETVYTIIPMPPIRFTKIFYNQONHVDSTGKFKHCNIPGLYFPAHYHTVYMKDVKYS 60

DB 509 FTAVLTSPPASGMPVRFRTLLNGHSGNVPATGISCPVGSVYFPAHYHVKGTWVA 568

QY 61 LFKKDKAMLETTYDOYQENNVDAQSGSVLLHLLEVGDQVWLQVYGEGERNGLYADNDSTF 120

DB 569 LYKNNVPATYTYDEYKKGVLDDQASGAVQLRPNDDVWVQIPSD-QANGLYSTREYIHSSP 627

QY 121 TGFLL 125

DB 628 SGFL 632

RESULT 12

hypothetical protein DKFZ586B0621.1 - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 20-Sep-1999 #sequence_rev1sion 20-Sep-1999 #text_change 09-Jul-2004

C:Accession: T14782

A:Title: The protein sequence database, August 1999

A:Reference number: Z18184

A:Accession: T14782

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-219 <ORT>

A:Cross-references: UNIPROT:Q9BXU0; EMBL:AL110261

A:Experimental source: adult uterus; clone DKFZ586B0621

C:Gene: DKFZ586B0621.1

Query Match

Best Local Similarity 34.4%; Score 243.5; DB 2; Length 219;

Matches 53; Conservative 23; Mismatches 45; Indels 5; Gaps 4;

QY 6 ETVYTIIPMPPIRFTKIFYNQONHVDSTGKFKHCNIPGLYFPAHYHTVYMKDVKYSLEK 64

DB 88 ESRVPPSPDAPLPFDVLYNVEGCHYDAVYKFTCYCPGYFPAHYHTVYMKDVKYSLEK 147

QY 65 DKAMLETTYDOYQENNVDAQSGSVLLHLLEVGDQVWLQVYGEGERNGLYADNDSTF 122

DB 148 GES-1ASFQFQFGMPKPSASLGSAMVRLEPEDQVWVQV-GVGDYIGIYASIKTDSFSG 205

QY 123 FLYYHD 128

DB 206 FLYYSD 211

RESULT 13

complement subcomponent C1q chain C precursor - human

N:Alternate names: complement subcomponent C1q gamma chain

C:Species: Homo sapiens (man)

C>Date: 22-May-1981 #sequence_rev1sion 31-May-1996 #text_change 09-Jul-2004

C:Accession: S14351; A03207

R:Sellar, G.C.; Blake, D.J.; Reid, K.B.M.

Biochem. J. 274, 481-490, 1991

A:Title: Characterization and organization of the genes encoding the A-, B- and C-chain

A:Reference number: S14350; PMID:91174759; PMID:1706597

A:Accession: S14351

A:Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-245 <SEL>

A:Cross-references: UNIPROT:P02747

R:Reid, K.B.M.

Biochem. J. 179, 367-371, 1979

A:Title: Complete amino acid sequences of the three collagen-like regions present in su-

A:Reference number: A90304; PMID:80020137; PMID:466087

A:Accession: A03207

A:Molecule type: protein

A:Residues: 29-56, 'P', 58-65, 'K', 67-71, 'P', 73-83, 'K', 85-86, 'D', 88-89, 'N', 91-122 <REI>

C:Comment: The first component of complement is a calcium-dependent complex of the three

ivation of C1r (enzyme), C1s (proenzyme), and the other eight components of complement.

dimers of the C1q subcomponent is composed of nine subunits, six of which are disulfid

A:Molecule type: mRNA

A:Residues: 1-219 <ORT>

A:Cross-references: UNIPROT:Q9BXU0; EMBL:AL110261

A:Experimental source: adult uterus; clone DKFZ586B0621

C:Gene: DKFZ586B0621.1

Query Match

Best Local Similarity 42.1%; Score 243.5; DB 2; Length 219;

Matches 53; Conservative 23; Mismatches 45; Indels 5; Gaps 4;

QY 6 ETVYTIIPMPPIRFTKIFYNQONHVDSTGKFKHCNIPGLYFPAHYHTVYMKDVKYSLEK 64

DB 88 ESRVPPSPDAPLPFDVLYNVEGCHYDAVYKFTCYCPGYFPAHYHTVYMKDVKYSLEK 147

QY 65 DKAMLETTYDOYQENNVDAQSGSVLLHLLEVGDQVWLQVYGEGERNGLYADNDSTF 122

DB 148 GES-1ASFQFQFGMPKPSASLGSAMVRLEPEDQVWVQV-GVGDYIGIYASIKTDSFSG 205

QY 123 FLYYHD 128

DB 206 FLYYSD 211

RESULT 13

complement subcomponent C1q chain C precursor - human

N:Alternate names: complement subcomponent C1q gamma chain

C:Species: Homo sapiens (man)

C>Date: 22-May-1981 #sequence_rev1sion 31-May-1996 #text_change 09-Jul-2004

C:Accession: S14351; A03207

R:Sellar, G.C.; Blake, D.J.; Reid, K.B.M.

Biochem. J. 274, 481-490, 1991

A:Title: Characterization and organization of the genes encoding the A-, B- and C-chain

A:Reference number: S14350; PMID:91174759; PMID:1706597

A:Accession: S14351

A:Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-245 <SEL>

A:Cross-references: UNIPROT:P02747

R:Reid, K.B.M.

Biochem. J. 179, 367-371, 1979

A:Title: Complete amino acid sequences of the three collagen-like regions present in su-

A:Reference number: A90304; PMID:80020137; PMID:466087

A:Accession: A03207

A:Molecule type: protein

A:Residues: 29-56, 'P', 58-65, 'K', 67-71, 'P', 73-83, 'K', 85-86, 'D', 88-89, 'N', 91-122 <REI>

C:Comment: The first component of complement is a calcium-dependent complex of the three

ivation of C1r (enzyme), C1s (proenzyme), and the other eight components of complement.

dimers of the C1q subcomponent is composed of nine subunits, six of which are disulfid

A:Molecule type: mRNA

A:Residues: 1-219 <ORT>

A:Cross-references: UNIPROT:Q9BXU0; EMBL:AL110261

A:Experimental source: adult uterus; clone DKFZ586B0621

C:Gene: DKFZ586B0621.1

Query Match

Best Local Similarity 30.9%; Score 219; DB 1; Length 245;

Matches 53; Conservative 22; Mismatches 47; Indels 8; Gaps 5;

QY 1 FSVGLTETVYTIIPMPPIRFTKIFYNQONHVDSTGKFKHCNIPGLYFPAHYHTVYMKDVKYS 59

DB 53 FSVGLTETVYTIIPMPPIRFTKIFYNQONHVDSTGKFKHCNIPGLYFPAHYHTVYMKDVKYS 59

QY 1 FSVGLTETVYTIIPMPPIRFTKIFYNQONHVDSTGKFKHCNIPGLYFPAHYHTVYMKDVKYS 59

DB 53 FSVGLTETVYTIIPMPPIRFTKIFYNQONHVDSTGKFKHCNIPGLYFPAHYHTVYMKDVKYS 59

QY 1 FSVGLTETVYTIIPMPPIRFTKIFYNQONHVDSTGKFKHCNIPGLYFPAHYHTVYMKDVKYS 59

DB 53 FSVGLTETVYTIIPMPPIRFTKIFYNQONHVDSTGKFKHCNIPGLYFPAHYHTVYMKDVKYS 59

QY 1 FSVGLTETVYTIIPMPPIRFTKIFYNQONHVDSTGKFKHCNIPGLYFPAHYHTVYMKDVKYS 59

DB 53 FSVGLTETVYTIIPMPPIRFTKIFYNQONHVDSTGKFKHCNIPGLYFPAHYHTVYMKDVKYS 59

QY 1 FSVGLTETVYTIIPMPPIRFTKIFYNQONHVDSTGKFKHCNIPGLYFPAHYHTVYMKDVKYS 59

DB 53 FSVGLTETVYTIIPMPPIRFTKIFYNQONHVDSTGKFKHCNIPGLYFPAHYHTVYMKDVKYS 59

QY 1 FSVGLTETVYTIIPMPPIRFTKIFYNQONHVDSTGKFKHCNIPGLYFPAHYHTVYMKDVKYS 59

DB 53 FSVGLTETVYTIIPMPPIRFTKIFYNQONHVDSTGKFKHCNIPGLYFPAHYHTVYMKDVKYS 59

QY 1 FSVGLTETVYTIIPMPPIRFTKIFYNQONHVDSTGKFKHCNIPGLYFPAHYHTVYMKDVKYS 59

DB 53 FSVGLTETVYTIIPMPPIRFTKIFYNQONHVDSTGKFKHCNIPGLYFPAHYHTVYMKDVKYS 59

QY 1 FSVGLTETVYTIIPMPPIRFTKIFYNQONHVDSTGKFKHCNIPGLYFPAHYHTVYMKDVKYS 59

DB 53 FSVGLTETVYTIIPMPPIRFTKIFYNQONHVDSTGKFKHCNIPGLYFPAHYHTVYMKDVKYS 59

QY 1 FSVGLTETVYTIIPMPPIRFTKIFYNQONHVDSTGKFKHCNIPGLYFPAHYHTVYMKDVKYS 59

DB 53 FSVGLTETVYTIIPMPPIRFTKIFYNQONHVDSTGKFKHCNIPGLYFPAHYHTVYMKDVKYS 59

QY 1 FSVGLTETVYTIIPMPPIRFTKIFYNQONHVDSTGKFKHCNIPGLYFPAHYHTVYMKDVKYS 59

DB 53 FSVGLTETVYTIIPMPPIRFTKIFYNQONHVDSTGKFKHCNIPGLYFPAHYHTVYMKDVKYS 59

QY 1 FSVGLTETVYTIIPMPPIRFTKIFYNQONHVDSTGKFKHCNIPGLYFPAHYHTVYMKDVKYS 59

DB 53 FSVGLTETVYTIIPMPPIRFTKIFYNQONHVDSTGKFKHCNIPGLYFPAHYHTVYMKDVKYS 59

QY 1 FSVGLTETVYTIIPMPPIRFTKIFYNQONHVDSTGKFKHCNIPGLYFPAHYHTVYMKDVKYS 59

DB 53 FSVGLTETVYTIIPMPPIRFTKIFYNQONHVDSTGKFKHCNIPGLYFPAHYHTVYMKDVKYS 59

QY 1 FSVGLTETVYTIIPMPPIRFTKIFYNQONHVDSTGKFKHCNIPGLYFPAHYHTVYMKDVKYS 59

DB 53 FSVGLTETVYTIIPMPPIRFTKIFYNQONHVDSTGKFKHCNIPGLYFPAHYHTVYMKDVKYS 59

QY 1 FSVGLTETVYTIIPMPPIRFTKIFYNQONHVDSTGKFKHCNIPGLYFPAHYHTVYMKDVKYS 59

DB 53 FSVGLTETVYTIIPMPPIRFTKIFYNQONHVDSTGKFKHCNIPGLYFPAHYHTVYMKDVKYS 59

QY 1 FSVGLTETVYTIIPMPPIRFTKIFYNQONHVDSTGKFKHCNIPGLYFPAHYHTVYMKDVKYS 59

DB 53 FSVGLTETVYTIIPMPPIRFTKIFYNQONHVDSTGKFKHCNIPGLYFPAHYHTVYMKDVKYS 59

QY 1 FSVGLTETVYTIIPMPPIRFTKIFYNQONHVDSTGKFKHCNIPGLYFPAHYHTVYMKDVKYS 59

Search completed: May 6, 2005, 17:30:49
Job time : 16.1497 secs

Db 122 FTVTRQTHQPPAPNSLIRFNAVLINPQGDYDTSTGKFTCKVGLYFYVHAS-HTANLCV 180
QY 60 SLFKKD-KAMLFTYDQYENNVDASGSVLLHLEVGDDQVYLQYGEGRNGLYXANDND 118
Db 181 LLYRSGVRYVFCGHTSKTNQVN--SGGVLLRLQVGEVWLAVNDYDMVGI---QSDS 235
QY 119 TETGFLYHD 128
Db 236 VFSGFLFPD 245

RESULT 14

A55797
collagen precursor, sacculle-specific - bluegill
C:Species: Lepomis macrochirus (bluegill)
C:Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 15-Sep-2003
C:Accession: A55797
R:Davis, J.G.; Oberholzer, J.C.; Burns, F.R.; Greene, M.I.
Science 267, 1031-1034, 1995
A:Title: Molecular cloning and characterization of an inner ear-specific structural prot
A:Reference number: A55797; PMID:95167486; PMID:7863331
A:Accession: A55797
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-423 <DAV>
A:Cross-references: GB:U17431; NID:G687605; PIDN:AAA6978.1; PID:G687606
F:58-271/Domain: collagenous, triple helix #status predicted <COL>
F:281-410/Domain: complement C1q carboxyl-terminal homology <C1Q>

Query Match

Best Local Similarity 30.9%; Score 219; DB 2; Length 423;
Matches 44; Conservative 17; Mismatches 39; Indels 2; Gaps 1;

QY 1 FSVGL-ETVTIPMPRTFKIFYNQNHDSGKFGHCNIPGLYFAHYHTVTKDVK 58
Db 282 FSVGLFSPRSPPPSLPVKFVFNCGHMDPTLNKNVTYPGVLYFSYHITYRNPVR 341
QY 59 VSLFKDKAMLFTYDQYENNVDASGSVLLHLEVGDDQVYLQ 100
Db 342 AALVNVGRKLRTRDLSLYGQDIDQASNLALHLTDDQVWLE 383

RESULT 15

S29328

Complement subcomponent C1q chain C - mouse

C:Species: Mus musculus (house mouse)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C:Accession: S29328

R:Petty, F.; Reid, K.B.M.; Loos, M.

Eur. J. Biochem. 209, 129-134, 1992

A:Title: Isolation, sequence analysis and characterization of cDNA clones coding for the

eectodeblin.

A:Reference number: S29328; MUID:93011118; PMID:1396691

A:Accession: S29328

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-246 <PRT>

A:Cross-references: UNIPROT:002105; EMBL:X66295; NID:G50228; PIDN:CAA46993.1; PID:G50229

C:Superfamily: complement subcomponent C1q chain A; complement C1q carboxyl-terminal hom

F:122-245/Domain: complement C1q carboxyl-terminal homology <C1Q>

Query Match

Best Local Similarity 29.4%; Score 208.5; DB 2; Length 246;
Matches 45; Conservative 23; Mismatches 43; Indels 5; Gaps 3;

QY 13 NMPIRFTKIFYNQNHDSGKFGHCNIPGLYFAHYHTVTKDVKSLFKDKAMLFY 72
Db 136 NALVRFNVSIVNPPQHTVNPSTGKFCVPGLYFYVY--TSHTANLCVHL-NUNLARVASF 193
QY 73 DQYQENNVDAQSGSVLLHLEVGDDQVYLQYGEGRNGLYXANDNDSTFTGFLYHD 128
Db 194 CDHMENSQVSSGGLRLRLRGDGVMLSV---NDYNGWVGIEGSNSVFSGFLFPD 246

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 6, 2005, 17:05:46 ; Search time 49.9028 Seconds

(without alignments)
1333.999 Million cell updates/sec

Title: US-10-072-159-11

Perfect score: 708

Sequence: 1 FSVGLERTYTYIPMPPIRFTK.....YADNNDSPFTGFLVHDIN 130

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	708	100.0	244	1 APM1_HUMAN	015848 homo sapien
2	707	99.9	243	2 Q95J17	095147 maccia mula
3	661	93.4	244	2 Q8K3R4	08K314 rattus norv
4	655	92.5	247	1 APM1_MOUSE	060994 mus musculu
5	655	92.5	247	2 Q8BRW2	08BRW2 mus musculu
6	633	89.4	244	2 Q76C76	076C76 canis fami
7	615	86.9	240	2 Q95M04	095M04 bos taurus
8	594	83.9	242	2 Q6Q2K6	06Q2K6 sus scrofa
9	594	83.9	243	2 Q6P07	06P07 sus scrofa
10	586	82.8	243	2 Q7YRF8	07YRF8 sus scrofa
11	557	78.7	244	2 Q6QWE7	06QWE7 gallus gall
12	514	72.6	242	2 Q95J95	095J95 canis fami
13	501	70.8	235	2 Q6GJ45	06GJ45 xenopus tro
14	478	67.5	235	2 Q6GJ45	06GJ45 xenopus tro
15	464	65.5	153	2 Q6GJ45	06GJ45 xenopus tro
16	445	58.6	144	2 Q6V9B4	06V9B4 sus scrofa
17	363	51.3	106	2 Q6ZV26	06ZV26 felis silve
18	355.5	50.2	333	2 Q81U04	081U04 homo sapien
19	345.5	48.8	195	2 Q8BZS3	08BZS3 mus musculu
20	310	43.8	145	2 Q6VPT9	06VPT9 sus scrofa
21	297.5	42.0	674	1 CAL1_CHICK	P08125 gallus gall
22	287.5	40.6	660	1 CAL1_HUMAN	Q03692 homo sapien
23	286	39.9	419	1 COLE_LEPMA	P98085 leptomis mac
24	282.5	39.9	675	2 Q9N178	Q9N178 sus scrofa
25	281.5	39.8	295	1 Q9N1K4	Q9N1K4 rattus norv
26	281	39.7	508	1 OTO1_ONCKE	P63371 oncorhynch
27	280.5	39.6	674	1 CAL1_BOVIN	P23206 bos taurus
28	280.5	39.6	660	1 CAL1_MOUSE	Q00306 mus musculu
29	280.5	39.6	743	1 CAL1_MOUSE	Q00780 mus musculu
30	280.5	39.6	744	2 Q921S8	Q921S8 mus musculu
31	280.5	39.6	744	2 Q8BGL6	Q8BGL6 m mus muscu

32	270.5	38.2	744	1 CAL1_HUMAN	P27658 homo sapien
33	267.5	37.8	744	1 CAL1_RABIT	P14282 oryctolagus
34	266.5	37.6	284	1 Q9D8U4	Q9D8U4 m mus muscu
35	265.5	37.5	285	1 Q9D8U4	Q9D8U4 m mus muscu
36	264.5	37.5	312	2 Q8CHX9	Q8CHX9 mus musculu
37	264.5	37.4	289	1 Q8CHX9	Q8CHX9 mus musculu
38	263.5	37.2	173	2 Q627B9	Q627B9 homo sapien
39	263.5	37.2	744	2 Q627B9	Q627B9 sus scrofa
40	258.5	36.5	102	2 Q95WB2	Q95WB2 gallus gall
41	258.5	36.5	170	1 CA28_MOUSE	Q95WB2 equus caball
42	257.5	36.4	640	2 Q6KAQ4	Q6KAQ4 mus musculu
43	257.5	36.4	643	2 Q6BED0	Q6BED0 mus musculu
44	257.5	36.4	699	2 Q6PIC4	Q6PIC4 mus musculu
45	256.5	36.2	289	2 Q8BVD7	Q8BVD7 mus musculu

ALIGNMENTS

RESULT 1	APM1_HUMAN	STANDARD;	PRT;	244 AA.
AC	Q15848;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	25-JAN-2005 (Rel. 46, Last annotation update)			
DE	Adiponectin precursor (Adipocyte, C1q and collagen domain containing protein) (30 kDa adipocyte complement-related protein) (ACRP30)			
DE	(Adipose most abundant gene transcript 1) (APM-1) (Gelatin-binding protein).			
GN	Name=ACDC; Synonyms=ACRP30, APM1, GBP28;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_Taxid=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=adipose tissue;			
RX	MEDLINE=96224171; PubMed=8619847; DOI=10.1006/dbrc.1996.0587;			
RA	Maeda K., Okubo K., Shimomura I., Funahashi T., Matsuzawa Y.,			
RA	Matsubara K.;			
RT	"cDNA cloning and expression of a novel adipose specific collagen-like factor, apm1 (adipose most abundant gene transcript 1).";			
RL	Biochem. Biophys. Res. Commun. 221:286-289(1996).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99196984; PubMed=10095105; DOI=10.1016/S0378-1119(99)00041-4;			
RA	Saito K., Tohe T., Minoshima S., Asakawa S., Sumiya J., Yoda M.,			
RA	Nakano Y., Shimizu N., Tomita M.;			
RT	"Organization of the gene for gelatin-binding protein (GBP28).";			
RL	Gene 229:67-73(1999).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99333693; PubMed=10403784; DOI=10.1006/dbrc.1999.0865;			
RA	Schaeffler A., Orso E., Palitzsch K.D., Buechler C., Drobnik W.,			
RA	Fueter A., Schoelmerich J., Schmitz G.;			
RT	"The human apm-1, an adipocyte-specific gene linked to the family of TNF's and to genes expressed in activated T cells, is mapped to chromosome 1q21.3-q23, a susceptibility locus identified for familial combined hyperlipidemia (FCH).";			
RL	Biochem. Biophys. Res. Commun. 260:416-425(1999).			
RN	[4]			
RP	SEQUENCE OF 19-33.			
RX	PubMed=15340161; DOI=10.1110/ps.04682504;			
RA	Zhang Z., Henzel W.J.;			
RT	"Signal peptide prediction based on analysis of experimentally verified cleavage sites.";			
RL	Protein Sci. 13:2819-2824(2004).			
RN	[5]			
RP	SEQUENCE OF N-TERMINUS, AND PARTIAL SEQUENCE.			
RX	PubMed=9947845;			
RA	Nakano Y., Tohe T., Choi-Miura N.H., Mazda T., Tomita M.;			
RT	"Isolation and characterization of GBP28, a novel gelatin-binding			

RT protein purified from human plasma.";
 RL J. Biochem. 120:803-812(1996).
 RN [6]
 RP CHARACTERIZATION.
 RX MEDLINE=20417747; PubMed=10961870;
 RA Yokota T., Oritani K., Takahashi I., Ishikawa J., Matsuyama A.,
 RA Ouchi N., Kihara S., Funahashi T., Tenner A.J., Tomiyama Y.,
 RA Matsuzawa Y.;
 RT "Adiponectin, a new member of the family of soluble defense collagens,
 RT negatively regulates the growth of myelomonocytic progenitors and the
 RT functions of macrophages.";
 RT Blood 96:1723-1732(2000).
 RN [7]
 RP CHARACTERIZATION.
 RX MEDLINE=20440368; PubMed=10982546;
 RA Ouchi N., Kihara S., Arita Y., Okamoto Y., Maeda K., Kuriyama H.,
 RA Hotta K., Nishida M., Takahashi M., Matsuguchi M., Ohmoto Y.,
 RA Nakamura T., Yamashita S., Funahashi T., Matsuzawa Y.;
 RT "Adiponectin, an adipocyte-derived plasma protein, inhibits
 RT endothelial NF-kappaB signaling through a CAMP-dependent pathway.";
 RT Circulation 102:1296-1301(2000).
 RN [8]
 RP FUNCTION.
 RX MEDLINE=21372498; PubMed=11479627; DOI=10.1038/90984;
 RA Yamauchi T., Kamon J., Waki H., Teranishi Y., Kubota N., Hara K.,
 RA Mori Y., Ide T., Murakami K., Tsuboyama-Kasaoka N., Ezaki O.,
 RA Akanuma Y., Gavrilova O., Vlasov C., Reitman M.L., Kagechika H.,
 RA Shudo K., Yoda M., Nakano Y., Tobe K., Nagai R., Kimura S., Tomita M.,
 RA Froguel P., Kadowaki T.;
 RT "The fat-derived hormone adiponectin reverses insulin resistance
 RT associated with both lipotrophy and obesity.";
 RT Nat. Med. 7:941-946(2001).
 RN [9]
 RP VARIANT ADIPONECTIN DEFICIENCY CVS-112.
 RX MEDLINE=20378830; PubMed=10918532;
 RA Takahashi M., Arita Y., Yamagata K., Matsukawa Y., Okutomi K.,
 RA Horie M., Shimomura I., Hotta K., Kuriyama H., Kihara S., Nakamura T.,
 RA Yamashita S., Funahashi T., Matsuzawa Y.;
 RT "Genomic structure and mutations in adipose-specific gene,
 RT adiponectin.";
 RT Int. J. Obes. Relat. Metab. Disord. 24:861-868(2000).
 RN [10]
 RP VARIANTS ARG-84; MET-117; THR-164; SER-221 AND PRO-241.
 RX MEDLINE=21671103; PubMed=11812766;
 RA Hare K., Boutin P., Mori Y., Tobe K., Kadowaki H., Hagura R., Akanuma Y.,
 RA Otobe S., Okada T., Eto K., Kadowaki K., Hara K., Yamauchi T.,
 RA Yazaki Y., Nagai R., Taniyama M., Matsubara K., Yoda M., Nakano Y.,
 RA Kimura S., Tomita M., Kimura S., Ito C., Froguel P., Kadowaki T.;
 RT "Genetic variation in the gene encoding adiponectin is associated with
 RT an increased risk of type 2 diabetes in the Japanese population.";
 RT Diabetes 51:536-540(2002).
 RN [11]
 RP FUNCTION: Important negative regulator in hematopoiesis and immune
 RN system; may be involved in ending inflammatory responses through
 RN its inhibitory functions. Inhibits endothelial NF-kappa-B
 RN signaling through a CAMP-dependent pathway. Inhibits TNF-alpha-
 RN induced expression of endothelial adhesion molecules. Involved in
 RN the control of fat metabolism and insulin sensitivity.
 RN [12]
 RP SUBUNIT: Homooligomer (Potential).
 RN [13]
 RP SUBCELLULAR LOCATION: Secreted.
 RN [14]
 RP TISSUE SPECIFICITY: Synthesized exclusively by adipocytes and
 RN secreted into plasma.
 RN [15]
 RP DISEASE: Defects in ADCD are the cause of adiponectin deficiency
 RN [MIM:605441]. The result is a very low concentration of plasma
 RN adiponectin. Decreased adiponectin plasma levels are associated
 RN with obesity, insulin resistance, and diabetes type 2.
 RN [16]
 RP PHARMACEUTICAL: Adiponectin might be used in the treatment of
 RN diabetes type 2 and insulin resistance.
 RN [17]
 RP SIMILARITY: Contains 1 C1q domain.
 RN [18]
 RP SIMILARITY: Contains 1 collagenous domain.
 RN [19]
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; D45371; BA08227.1; -;
 CC EMBL; AB012165; BA086716.1; -;
 CC EMBL; AB012164; BA086716.1; JOINED.
 CC EMBL; AJ131460; CAB52413.1; -;
 CC EMBL; AJ131461; CAB52413.1; JOINED.
 CC PIR; JG4708; JG4708.
 CC HSBP; O60994; IC28.
 CC Genew; HGNC:13633; ADCD.
 CC MIM; 605441; -;
 CC GO; GO:0006091; P:energy pathways; TMS.
 CC InterPro; IPR01073; C1q.
 CC InterPro; IPR008161; C1q helix.
 CC InterPro; IPR008160; Collagen.
 CC InterPro; IPR008983; TNF-like.
 CC Pfam; PF00386; C1q; 1.
 CC Pfam; PF01391; Collagen; 1.
 CC PRINTS; PR00007; COMPLEMENTC1Q.
 CC PRODOM; PD000007; C1q_helix; 2.
 CC PROSITE; PS50871; C1Q; 1.
 CC Collagen; Diabetes mellitus; Direct protein sequencing;
 CC Disease mutation; Hormone; Hydroxylation; Obesity; Plasma;
 CC Polymorphism; Repeat; Signal.
 CC SIGNAL 1 18
 CC CHAIN 1 18
 CC FT 19 244 Adiponectin.
 CC FT DOMAIN 42 107 Collagen-like.
 CC FT 108 244 C1q.
 CC FT DISULFID 36 36 Interchain (By similarity).
 CC FT MOD_RES 44 44 4-hydroxyproline (By similarity).
 CC FT MOD_RES 47 47 4-hydroxyproline (By similarity).
 CC FT MOD_RES 53 53 4-hydroxyproline (By similarity).
 CC FT MOD_RES 62 62 4-hydroxyproline (By similarity).
 CC FT MOD_RES 71 71 4-hydroxyproline (By similarity).
 CC FT MOD_RES 76 76 4-hydroxyproline (By similarity).
 CC FT MOD_RES 86 86 4-hydroxyproline (By similarity).
 CC FT MOD_RES 95 95 4-hydroxyproline (By similarity).
 CC FT MOD_RES 104 104 4-hydroxyproline (By similarity).
 CC FT CARBOHYD 230 230 N-linked (GlcNAc...) (Potential).
 CC FT VARIANT 84 84 G->R.
 CC FT VARIANT 112 112 /FTid=VAR_013273.
 CC FT VARIANT 117 117 R->C (in adiponectin deficiency).
 CC FT VARIANT 164 164 /FTid=VAR_013274.
 CC FT VARIANT 164 164 V->M.
 CC FT VARIANT 164 164 /FTid=VAR_013275.
 CC FT VARIANT 221 221 I->T.
 CC FT VARIANT 221 221 /FTid=VAR_013276.
 CC FT VARIANT 241 241 R->S.
 CC FT VARIANT 241 241 /FTid=VAR_013277.
 CC FT VARIANT 241 241 H->P.
 CC FT SEQUENCE 244 AA; 26414 MW; 64D86C1204B1018 CRC64;
 CC SQ
 CC Query Match 100.0%; Score 708; DB 1; Length 244;
 CC Best local similarity 100.0%; Pred. No. 5; le-62;
 CC Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 1 FSVGLETVYVTPNPNPIRTKIFYNQNNHYDSTGKFKHCNIPGLYFAVHTVYMKDVYS 60
 CC DB 115 FSVGLETVYVTPNPNPIRTKIFYNQNNHYDSTGKFKHCNIPGLYFAVHTVYMKDVYS 174
 CC QY 61 LFKDKAMLFYDYQENNVDAAGSVTLHLEVGDWLQVYGGERNGLYADNDNSTF 120
 CC DB 175 LFKDKAMLFYDYQENNVDAAGSVTLHLEVGDWLQVYGGERNGLYADNDNSTF 234
 CC QY 121 TGFLLYHDTN 130
 CC DB 235 TGFLLYHDTN 244

RESULT 2
Q95JD7 PRELIMINARY; PRT; 243 AA.
AC Q95JD7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Adiponectin.
GN Name=APM1;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Adipose;
MEDLINE=21322234; PubMed=11334417;
RA Hotta K., Funahashi T., Bodkin N.L., Ortmeier H.K., Arlt A.Y., Hansen B.C., Matsuzawa Y.;
RA "Circulating concentrations of the adipocyte protein adiponectin are decreased in parallel with reduced insulin sensitivity during the progression in parallel with reduced insulin sensitivity during the RT diabetes 50:1126-1133(2001)."
RL EMBL; AF404407; AAK92202.1; -
DR HSSP; Q60994; 1C28.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0006817; P:phosphate transport; IEA.
DR InterPro; IPR001073; Clq.
DR InterPro; IPR008161; Clq_helix.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR008983; TNF_like.
DR Pfam; PF00386; Clq; 1.
DR Pfam; PF01391; Collagen; 1.
DR PRINTS; PR00007; COMPLEMENTC1Q.
DR PRODOM; PD000007; Clq_helix; 1.
DR SMART; SM00110; Clq; 1.
DR PROSITE; PS01113; Clq; 1.
KW Collagen.
SQ SEQUENCE 243 AA; 26264 MW; 49A45DAF2B613FD CRC64;
Query Match 99.3%; Score 707; DB 2; Length 243;
Best Local Similarity 99.2%; Pred. No. 6.4e-62;
Matches 129; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 FSVGLETVYVTPMPPIRFTKIFYNQONHYDSTGKFKHCNIPGLYFYFAHYHTVYMKDVKS 60
DB 114 FSVGLETVYVTPMPPIRFTKIFYNQONHYDSTGKFKHCNIPGLYFYFAHYHTVYMKDVKS 173
QY 61 LFKKDXAMLFYDYQYENNVDAAGSVLLHLEVDQVWLQVYEGEGNGLYADNDSTF 120
DB 174 LFKKDXAMLFYDYQYENNVDAAGSVLLHLEVDQVWLQVYEGEGNGLYADNDSTF 233
QY 121 TGFLLYHDTN 130
DB 234 TGFLLYHDTN 243

RA Berg A.H., Scherer P.E.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; AY033865; AAK61608.1; -
DR HSSP; Q60994; 1C28.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0006817; P:phosphate transport; IEA.
DR InterPro; IPR001073; Clq.
DR InterPro; IPR008161; Clq_helix.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR008983; TNF_like.
DR Pfam; PF00386; Clq; 1.
DR Pfam; PF01391; Collagen; 1.
DR PRINTS; PR00007; COMPLEMENTC1Q.
DR PRODOM; PD000007; Clq_helix; 2.
DR SMART; SM00110; Clq; 1.
DR PROSITE; PS01113; Clq; 1.
KW Collagen.
SQ SEQUENCE 244 AA; 26410 MW; 75B2B1DF68E2633E CRC64;
Query Match 93.4%; Score 661; DB 2; Length 244;
Best Local Similarity 92.3%; Pred. No. 2.3e-57;
Matches 120; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
QY 1 FSVGLETVYVTPMPPIRFTKIFYNQONHYDSTGKFKHCNIPGLYFYFAHYHTVYMKDVKS 60
DB 115 FSVGLETVYVTPMPPIRFTKIFYNQONHYDSTGKFKHCNIPGLYFYFAHYHTVYMKDVKS 174
QY 61 LFKKDXAMLFYDYQYENNVDAAGSVLLHLEVDQVWLQVYEGEGNGLYADNDSTF 120
DB 175 LFKKDXAMLFYDYQYENNVDAAGSVLLHLEVDQVWLQVYEGEGNGLYADNDSTF 234
QY 121 TGFLLYHDTN 130
DB 235 TGFLLYHDTN 244

RESULT 4
APM1_MOUSE STANDARD; PRT; 247 AA.
ID APM1_MOUSE
AC Q60994; Q62400; Q9DC68;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Adiponectin precursor (Adipocyte, Clq and collagen domain containing protein) (30 kDa adipocyte complement-related protein) (ACRP30)
DE (Adipocyte specific protein AdipoQ).
GN Name=Acad; Synonyms=Acprp30, Adipoq, Apm1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Adipocyte;
RX MEDLINE=96070757; PubMed=7592907; DOI=10.1074/jbc.270.45.26746;
RA Scherer P.E., Williams S., Fogliano M., Baldini G., Lodish H.F.;
RT "A novel serum protein similar to Clq, produced exclusively in adipocytes."
RL J. Biol. Chem. 270:26746-26749 (1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Adipocyte;
RX MEDLINE=11162643; DOI=10.1006/dbrc.2001.4217;
RA Das K., Lin Y., Widen E., Zhang Y., Scherer P.E.;
RT "Chromosomal localization, expression pattern, and promoter analysis of the mouse gene encoding adipocyte-specific secretory protein Acrp30."
RN [3]
RP SEQUENCE FROM N.A.
RX PubMed=11162643; DOI=10.1006/dbrc.2001.4217;
RA Das K., Lin Y., Widen E., Zhang Y., Scherer P.E.;
RT "Chromosomal localization, expression pattern, and promoter analysis of the mouse gene encoding adipocyte-specific secretory protein Acrp30.";

RL Biochem. Biophys. Res. Commun. 280:1120-1129 (2001).
[4]
RA SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Heart;
RX MEDLINE=223546683; PubMed=12466651; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nixaidi I., Oato N., Saito R., Suzuki H., Yamana K.I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gotohori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schmitt L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chochia C., Corbani L.E., Cousins S.,
RA Dalla E., Dregant T.A., Fletcher C.F., Forrest A., Frizer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gusninch S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.W., King B.L.,
RA Kionaga A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Nunata K., Okido T., Pavan W.J., Perlea G., Pesole G.,
RA Petrovskiy N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sadelain A., Schneider C., Sempke C.A., Setou M., Shlnada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wysshaw-Borje A., Yamaizawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carinini P., Hayatsu N.,
RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Seto K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Aizawa T., Fukuda S.,
RA Hara A., Hashizume W., Imocani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sakai D., Shibata K., Shingawa A.,
RA Yamanishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
[5]
RN FUNCTION.
RP MEDLINE=21372498; PubMed=11479627; DOI=10.1038/90984;
RX Yamauchi T., Kamon J., Waki H., Teranishi Y., Kubota N., Hara K.,
RA Mori Y., Ide T., Murakami K., Tsuboyama-Kasaoka N., Ezaki O.,
RA Akanuma Y., Gavrilova O., Vlassara C., Reitman M.L., Kagechika H.,
RA Shudo K., Yoda M., Nakano Y., Tobe K., Nagai R., Kimura S., Tomita M.,
RA Froguel P., Kadookari T.;
RT "The fat-derived hormone adiponectin reverses insulin resistance
RT associated with both lipotrophy and obesity."
RL Nat. Med. 7:941-946(2001).
[6]
RN FUNCTION.
RP MEDLINE=21372499; PubMed=11479628; DOI=10.1038/90992;
RX Berg A.H., Combs T.P., Du X., Brownlee M., Scherer P.E.;
RA "The adipocyte-secreted protein Acrp30 enhances hepatic insulin
RT action."
RL Nat. Med. 7:947-953 (2001).
[7]
CC -FUNCTION: Important negative regulator in hematopoiesis and immune
CC systems; may be involved in ending inflammatory responses through
CC its inhibitory functions. Inhibits endothelial NF-kappa-B
CC signaling through a cAMP-dependent pathway. Inhibits TNF-alpha-
CC induced expression of endothelial adhesion molecules. Involved in
CC the control of fat metabolism and insulin sensitivity.
CC -SUBUNIT: Homooligomer.
CC -SUBCELLULAR LOCATION: Secreted.
CC -TISSUE SPECIFICITY: Synthesized exclusively by adipocytes and
CC secreted into plasma.
CC -INDUCTION: During hormone-induced adipose differentiation and
CC activated by insulin.
CC -SIMILARITY: Contains 1 C1q domain.
CC -SIMILARITY: Contains 1 collagenous domain.
CC -----
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DR      EMBL, U37222; AAA80543.1; -.
DR      EMBL, U4915; AAB06706.1; -.
DR      EMBL, AF304466; AAK13417.1; -.
DR      EMBL, AK003138; BAB22597.1; -.
DR      PDB, 1C28; X-ray; A/B/C-113-246.
DR      PDB, 1C3H; X-ray; A/B/C/D/E/F=111-247.
DR      MGI, MGI:106675; Acdc.
DR      GO; GO:0005576; C:extracellular; IDA.
DR      GO; GO:0005515; F:protein binding; IPI.
DR      GO; GO:0006635; P:fatty acid beta-oxidation; IMP.
DR      InterPro; IPRO01073; Clq.
DR      InterPro; IPRO08161; Clq helix.
DR      InterPro; IPRO08160; Collagen.
DR      InterPro; IPRO08983; TNF-like.
DR      Pfam; PF00386; Clq; 1.
DR      Pfam; PF01391; Collagen; 1.
DR      PRINTS; PR00007; COMPLEMENTC1Q.
DR      ProDom; PD000007; Clq_helix; 2.
DR      SMART; SM00110; Clq; 1.
DR      PROSITE; PS00871; Clq; 1.
KW      3D-structure; Collagen; Hormone; Hydroxylation; Plasma; Polymorphism;
KW      Repeat; Signal.
FT      SIGNAL          1      17      Potential.
FT      CHAIN           18      247      Adiponectin.
FT      DOMAIN          45      110      Collagen-like.
FT      DOMAIN          111     247      Clq.
FT      DISULFID        39      39      Interchain (By similarity).
FT      MOD_RES         47      47      4-hydroxyproline (By similarity).
FT      MOD_RES         50      50      4-hydroxyproline (By similarity).
FT      MOD_RES         56      56      4-hydroxyproline (By similarity).
FT      MOD_RES         65      65      4-hydroxyproline (By similarity).
FT      MOD_RES         79      79      4-hydroxyproline (By similarity).
FT      MOD_RES         98      98      4-hydroxyproline (By similarity).
FT      MOD_RES        107     107      4-hydroxyproline (By similarity).
FT      CARBOHYD        233     233      N-linked (GlcNAc...) (Potential).
FT      VARIANT         113     113      M -> V.
FT      CONFLICT        50      50      P -> S (in Ref. 2).
FT      CONFLICT        74      74      A -> S (in Ref. 2).
FT      CONFLICT       117     117      A -> G (in Ref. 2).
FT      CONFLICT       148     148      G -> N (in Ref. 2).
FT      CONFLICT       243     243      Y -> F (in Ref. 2).
SQ      SEQUENCE        247 AA; 26841 MW; 137B687D873986C4 C=CC64;

Query Match          92.5%; Score 655; DB 1; Length 247;
Best Local Similarity 91.5%; Pred. No. 9.3e-57;
Matches 119; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY      1 FSVGLEIYVITENMPIRFTKIFVNOQNHYSSTGKFKHCNITGLYFAVHIVYMKDVYS 60
      |||||
DB      118 FSVGLEIRVIVPNVPIRFTKIFVNOQNHYSSTGKFKYCNIPGLYFYSYHIVYMKDVYS 177
      |||||

QY      61 LFKKDKMLFFPYDYOENNVDOASGSYTLHLEVGDQWLVGYGGBERGGLYADNDNDSTF 120
      |||||
DB      178 LFKKDKVLFVYDDYQEKVNDASGSYTLHLEVGDQWLVGYGGBDNGHGLYADNDVNSTF 237
      |||||

QY      121 TGFLLYHDTN 130
      |||||
DB      238 TGFLLYHDTN 247

RESULT 5
O8BRW2 PRELIMINARY; PRT; 247 AA.
AC O8BRW2.
DT 01-MAR-2003 (TRENBLREL. 23, Created)
DT 01-MAR-2003 (TRENBLREL. 23, Last sequence update)
DT 01-OCT-2003 (TRENBLREL. 25, Last annotation update)
DE Mus musculus adult male aorta and vein cDNA, RIKEN full-length
DE enriched library, clone:A530909P11 product:adipocyte complement
DE related protein of 30 kDa, full insert sequence.
GN Name=Acdc;

```

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RX STRAIN=C57BL/6J; TISSUE=Aorta and vein;
 RX MEDLINE=9279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA RIKEN PANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
 RA The PANTOM Consortium;
 RT the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Katsunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Matshiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuda S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoaka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohnaka N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takada Y., Tanaka T.,
 RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RL EMBL; A004214; BAC30866.1; -.
 DR HSSP; Q60994; IC28.
 DR MGD; MGI:106675; Acde.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0005179; F:hormone activity; TAS.
 DR GO; GO:0005515; F:protein binding; IPT.
 DR GO; GO:0006635; P:fatty acid beta-oxidation; IMP.
 DR GO; GO:0006006; P:glucose metabolism; IDA.
 DR InterPro; IPR001073; Clq.

DR InterPro; IPR008161; Clq_helix.
 DR InterPro; IPR008160; Collagen.
 DR InterPro; IPR008983; TNF_like.
 DR Pfam; PF00386; Clq; 1.
 DR Pfam; PF01391; Collagen_1.
 DR PRINTS; PR00007; COMPLEMENTC1Q.
 DR PRODOM; PD000007; Clq_helix; 1.
 DR SMART; SM00110; Clq; 1.
 DR PROSITE; PS01113; Clq; 1.
 KW Collagen.
 SQ SEQUENCE 247 AA; 26751 MW; 0D3FA64C789CAEF3 CRC64;
 Query Match 92.5%; Score 655; DB 2; Length 247;
 Best Local Similarity 91.5%; Pred. No. 9, 3e-57;
 Matches 119; Conservative 7; Mismatches 4; Indels 0; Gaps 0;
 QY 1 FSVGLTETVTTPMIRFTKIRYNOQNHSDSTGKFKCNIPGLYFAHYHITVMKDVKS 60
 DB 118 FSVGLETRVTVPNVPFRFTKIRYNOQNHSDSTGKFCNIPGLYFSAHYITVMKDVKS 177
 QY 61 LFKKKAMLFYDQGVENNVDASGSLHLLEVGDQVWLQVYGEGRNGLYADNDNSTF 120
 DB 178 LFKKDAVLFYDQGVENVDASGSLHLLEVGDQVWLQVYGDGSHNGLYADNDNSTF 237
 QY 121 TGFLLYHDTN 130
 DB 238 TGFLLYHDTN 247
 RESULT 6
 QY 076C76 PRELIMINARY; PRT; 244 AA.
 AC 076C76;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Adiponectin.
 GN Name=apML;
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 ON NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ishioaka K., Omachi A., Sagawa M., Shibata H., Honjoh T., Kimura K.,
 RA Saito M.;
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB110099; BAD15362.1; -.
 DR GO; GO:0005737; C:cycloplasm; IEA.
 DR GO; GO:0006817; P:phosphate transport; IEA.
 DR InterPro; IPR001073; Clq.
 DR InterPro; IPR008161; Clq_helix.
 DR InterPro; IPR008160; Collagen.
 DR InterPro; IPR008983; TNF_like.
 DR Pfam; PF00386; Clq; 1.
 DR Pfam; PF01391; Collagen_1.
 DR PRINTS; PR00007; COMPLEMENTC1Q.
 DR PRODOM; PD000007; Clq_helix; 1.
 DR SMART; SM00110; Clq; 1.
 DR PROSITE; PS01113; Clq; 1.
 KW collagen.
 SQ SEQUENCE 244 AA; 26361 MW; 58659B7CC8865FB8 CRC64;
 Query Match 89.4%; Score 633; DB 2; Length 244;
 Best Local Similarity 86.9%; Pred. No. 1, 4e-54;
 Matches 113; Conservative 11; Mismatches 6; Indels 0; Gaps 0;
 QY 1 FSVGLETTVTTPMIRFTKIRYNOQNHSDSTGKFKCNIPGLYFAHYHITVMKDVKS 60
 DB 115 FSVGLESTRVTVPNVPFRFTKIRYNOQNHSDSTGKFKCNIPGLYFSAHYITVMKDVKS 174
 QY 61 LFKKKAMLFYDQGVENNVDASGSLHLLEVGDQVWLQVYGEGRNGLYADNDNSTF 120

Db 175 LYKDKKAMLFYDYQYQKKNVDQASGSVLLHLEVGQVWLQVYGGDSXGYADNVNDSTF 234
QY 121 TGFLLYHDTN 130
Db 235 TGFLLYHDTN 244

RESULT 7

Q95M04

ID Q95M04 PRELIMINARY; PRT; 240 AA.

AC Q95M04 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Adipose tissue-specific protein adipo Q.
OS Bos taurus (Bovine)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21369933; PubMed=11382781; DOI=10.1074/jbc.M104148200;
RA Sato C., Yasukawa Z., Honda N., Matsuda T., Kitaajima K.;
RT "Identification and adipocyte differentiation-dependent expression of
RT the unique dialytic acid residue in an adipose tissue-specific
RT glycoprotein, adipo Q."
RL J. Biol. Chem. 276:28849-28856(2001).
DR EMBL; AF269230; AAKS8902.1; -.
DR HSSP; Q60994; 1C28.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0006817; P:phosphate transport; IEA.
DR InterPro; IPR01073; Clq.
DR InterPro; IPR008161; Clq_helix.
DR InterPro; IPR008160; Collagen.
DR Pfam; PF00386; Clq_1.
DR Pfam; PF01391; Collagen; 1.
DR PRINTS; PR00007; COMPLEMENTC1Q.
DR ProDom; PD000007; Clq_helix; 2.
DR SMART; SM00110; Clq; 1.
DR PROSITE; PS01113; Clq; 1.
KW Collagen.
SQ SEQUENCE 240 AA; 26091 MW; C6253BA803BA668 CRC64;

Query Match 86.9%; Score 615; DB 2; Length 240;
Best Local Similarity 89.9%; Pred. No. 8.3e-53;
Matches 116; Conservative 7; Mismatches 4; Indels 2; Gaps 2;

QY 1 FSVGLETVYTIIPNMPIRFTKIFVYQNNHYDSTGKFKHCNIPGLYFAVHITVYMKDVKVS 60
Db 110 FSVGLETVYTIIPNMPIRFTKIFVYQNNHYDSTGKFKHCNIPGLYFAVHITVYMKDVKVS 169
QY 61 LFKDKKAMLFYDYQYQKKNVDQASGSVLLHLEVGQVWLQVYGGDSXGYADNVNDSTF 119
Db 170 LFKDKKAMLFYDYQYQKKNVDQASGSVLLHLEVGQVWLQVY-EGENNGVYADNVNDST 228
QY 120 FTGFLYHDTN 128
Db 229 FTGFLYHDTN 237

RESULT 8

Q6Q2K6

ID Q6Q2K6 PRELIMINARY; PRT; 242 AA.

AC Q6Q2K6 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Adiponectin (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI_TaxID=9623;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang G., Yang Z.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY563526; AAS75592.1; -.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0006817; P:phosphate transport; IEA.
DR InterPro; IPR001073; Clq.
DR InterPro; IPR008161; Clq_helix.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR008983; TNF_like.
DR Pfam; PF00386; Clq; 1.
DR Pfam; PF01391; Collagen; 1.
DR PRINTS; PR00007; COMPLEMENTC1Q.
DR ProDom; PD000007; Clq_helix; 2.
DR SMART; SM00110; Clq; 1.
DR PROSITE; PS01113; Clq; 1.
KW Collagen.
FT NON TER
SQ SEQUENCE 242 AA; 26265 MW; 1F3284A902E87D6D CRC64;

Query Match 83.9%; Score 594; DB 2; Length 242;
Best Local Similarity 83.6%; Pred. No. 1e-50;
Matches 107; Conservative 12; Mismatches 9; Indels 0; Gaps 0;

QY 1 FSVGLETVYTIIPNMPIRFTKIFVYQNNHYDSTGKFKHCNIPGLYFAVHITVYMKDVKVS 60
Db 113 FSVGLETVYTIIPNMPIRFTKIFVYQNNHYDSTGKFKHCNIPGLYFAVHITVYMKDVKVS 172
QY 61 LFKDKKAMLFYDYQYQKKNVDQASGSVLLHLEVGQVWLQVYGGDSXGYADNVNDSTF 120
Db 173 LFKDKKAMLFYDYQYQKKNVDQASGSVLLHLEVGQVWLQVYGGDSXGYADNVNDSTF 232
QY 121 TGFLLYHDTN 128
Db 233 TGFLLYHDTN 240

RESULT 9

Q6P07

ID Q6P07 PRELIMINARY; PRT; 243 AA.

AC Q6P07 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Adiponectin.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9623;
RN [1]
RP SEQUENCE FROM N.A.
RA Chuang C.J., Liu B.H., Ding S.T.;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY589691; AAT00459.1; -.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0006817; P:phosphate transport; IEA.
DR InterPro; IPR01073; Clq.
DR InterPro; IPR001073; Clq.
DR InterPro; IPR008161; Clq_helix.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR008983; TNF_like.
DR Pfam; PF00386; Clq; 1.
DR Pfam; PF01391; Collagen; 1.
DR PRINTS; PR00007; COMPLEMENTC1Q.
DR ProDom; PD000007; Clq_helix; 2.
DR SMART; SM00110; Clq; 1.
DR PROSITE; PS01113; Clq; 1.
KW Collagen.
SQ SEQUENCE 243 AA; 26370 MW; B886026A3C7C4474 CRC64;

Query Match 83.9%; Score 594; DB 2; Length 243;
Best Local Similarity 83.6%; Pred. No. 1e-50;

Matches 107; Conservative 12; Mismatches 9; Indels 0; Gaps 0;

QY 1 FSVGLTYYTIPMPPIRFTKIFYNQONHYDSTGKFKHCNIPGLYFAYHITVYMKDKVKS 60
 DB 114 FSVGLTYYTIPMPPIRFTKIFYNQONHYDSTGKFKHCNIPGLYFAYHITVYMKDKVKS 173
 QY 61 LFKKDXAMLFYDQYQENNVDAQSGSVLHLLEVGDQVWLQVYEGEENGGLYADNDSTF 120
 DB 174 LFKKDXAMLFYDQYQENNVDAQSGSVLHLLEVGDQVWLQVYEGEENGGLYADNDSTF 233
 QY 121 TGFLLYHD 128
 DB 234 TGFLLYHN 241

RESULT 10

QYRF8 PRELIMINARY; PRT; 243 AA.
 AC 07YRF8
 DT 01-OCT-2003 (TREMBlrel. 25, Created)
 DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Adiponectin.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ledoux S.L., Murphy B.D.;
 RL Submitted (JCT-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY135647; AN11297.2; -.
 DR HSSP: Q60994; 1C28.
 DR GO: GO:0005737; Cytoplasm; IEA.
 DR GO: GO:0006817; P:phosphate transport; IEA.
 DR InterPro: IPR001073; Clq.
 DR InterPro: IPR008161; Clq_helix.
 DR InterPro: IPR008160; Collagen.
 DR InterPro: IPR008983; TNF_like.
 DR Pfam: PF00386; Clq; 1.
 DR Pfam: PF01391; Collagen; 1.
 DR PRINTS: PRO0007; COMPLEMENTC1Q.
 DR ProDom: PD000007; Clq_helix; 1.
 DR SMART: SM00110; Clq; 1.
 KW Collagen.
 SQ SEQUENCE 243 AA; 26367 MW; 440D1B2BF29738E CRC64;

Query Match 82.8%; Score 586; DB 2; Length 243;
 Best Local Similarity 82.0%; Pred. No. 6,3e-50;
 Matches 105; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

QY 1 FSVGLTYYTIPMPPIRFTKIFYNQONHYDSTGKFKHCNIPGLYFAYHITVYMKDKVKS 60
 DB 114 FSVGLTYYTIPMPPIRFTKIFYNQONHYDSTGKFKHCNIPGLYFAYHITVYMKDKVKS 173
 QY 61 LFKKDXAMLFYDQYQENNVDAQSGSVLHLLEVGDQVWLQVYEGEENGGLYADNDSTF 120
 DB 174 LFKKDXAMLFYDQYQENNVDAQSGSVLHLLEVGDQVWLQVYEGEENGGLYADNDSTF 233
 QY 121 TGFLLYHD 128
 DB 234 TGFLLYHN 241

RESULT 11

QYRF8 PRELIMINARY; PRT; 244 AA.
 AC 06QWE7;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Adiponectin.
 OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yuan J., Liu W., Liu Z., Li N.;
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY523537; MAS67924.1; -.
 DR GO: GO:0005737; Cytoplasm; IEA.
 DR GO: GO:0006817; P:phosphate transport; IEA.
 DR InterPro: IPR001073; Clq.
 DR InterPro: IPR008161; Clq_helix.
 DR InterPro: IPR008160; Collagen.
 DR InterPro: IPR008983; TNF_like.
 DR Pfam: PF00386; Clq; 1.
 DR Pfam: PF01391; Collagen; 1.
 DR PRINTS: PRO0007; COMPLEMENTC1Q.
 DR ProDom: PD000007; Clq_helix; 1.
 DR SMART: SM00110; Clq; 1.
 DR PROSITE: PS01113; Clq; 1.
 KW Collagen.
 SQ SEQUENCE 244 AA; 26461 MW; 72DEBD36385C49DD CRC64;

Query Match 78.7%; Score 557; DB 2; Length 244;
 Best Local Similarity 77.7%; Pred. No. 4.8e-47;
 Matches 101; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

QY 1 FSVGLTYYTIPMPPIRFTKIFYNQONHYDSTGKFKHCNIPGLYFAYHITVYMKDKVKS 60
 DB 113 FSVGLTYYTIPMPPIRFTKIFYNQONHYDSTGKFKHCNIPGLYFAYHITVYMKDKVKS 172
 QY 61 LFKKDXAMLFYDQYQENNVDAQSGSVLHLLEVGDQVWLQVYEGEENGGLYADNDSTF 120
 DB 173 LFKKDXAMLFYDQYQENNVDAQSGSVLHLLEVGDQVWLQVYEGEENGGLYADNDSTF 232
 QY 121 TGFLLYHD 130
 DB 233 TGFLLYPTD 242

RESULT 12

QYRF8 PRELIMINARY; PRT; 194 AA.
 AC 095J95;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Adiponectin (Fragment).
 GN Name=APM1;
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA TISSUE=Adipose;
 RC Kabir M., Ananthanarayan S., Ionut V., Kim S.P., Van Citters G.W.,
 RA Dea M.K., Bergman R.N.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF417206; AAL09702.1; -.
 DR HSSP: Q60994; 1C28.
 DR GO: GO:0005737; Cytoplasm; IEA.
 DR GO: GO:0006817; P:phosphate transport; IEA.
 DR InterPro: IPR001073; Clq.
 DR InterPro: IPR008161; Clq_helix.
 DR InterPro: IPR008160; Collagen.
 DR InterPro: IPR008983; TNF_like.
 DR Pfam: PF00386; Clq; 1.
 DR Pfam: PF01391; Collagen; 1.
 DR PRINTS: PRO0007; COMPLEMENTC1Q.
 DR ProDom: PD000007; Clq_helix; 1.
 DR SMART: SM00110; Clq; 1.

DR PROSITE; PS01113; C1Q; 1.
KW Collagen.
FT NON TER 1 1
FT NON TER 194 194
SQ SEQUENCE 194 AA; 20890 MW; 3AA3D947D187AF9A CRC64;
Query Match 72.6%; Score 514; DB 2; Length 194;
Best Local Similarity 89.3%; Pred. No. 6,8e-43;
Matches 92; Conservative 8; Mismatches 3; Indels 0; Gaps 0;
QY 1 FSVGLFTVITPNNPIRFTKIFVNOQNHVDSGTGKFGHCNIPGLYFAVHITVYMKDVYVS 60
DB 92 FSVGLSRTVPPNVPIRFTKIFVNOQNHVDSGTGKFGHCNIPGLYFAVHITVYMKDVYVS 151
QY 61 LFKDKAMLFYTDYOENNVDSAGSVLLHLEVGQVWLQVYVG 103
DB 152 LFKDKAMLFYTDYOENNVDSAGSVLLHLEVGQVWLQVYVG 194
RESULT 13
06DJ45
ID 06DJ45 PRELIMINARY; PRT; 235 AA.
AC 06DJ45;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Col1a1-prov protein.
GN Name=col1a1-prov;
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8364;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shennen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gamaralle P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzyniński M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=whole body;
RA Klein S., Gerhard D.S.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC075339; AAH75339.1; -.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0006817; P:phosphate transport; IEA.
DR InterPro; IPR001073; C1Q.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR008983; TNF1like.
DR Pfam; PF00386; C1Q; 1.
DR Pfam; PF03391; Collagen.1.
DR PRINTS; PR00007; COMPLEMENTC1Q.
DR SMART; SM00110; C1Q; 1.
DR PROSITE; PS01113; C1Q; 1.

KW Collagen.
SQ SEQUENCE 235 AA; 25562 MW; 558275AA3C872A32 CRC64;
Query Match 70.8%; Score 501; DB 2; Length 235;
Best Local Similarity 68.8%; Pred. No. 1.6e-41;
Matches 88; Conservative 20; Mismatches 20; Indels 0; Gaps 0;
QY 1 FSVGLFTVITPNNPIRFTKIFVNOQNHVDSGTGKFGHCNIPGLYFAVHITVYMKDVYVS 60
DB 108 FSVGLSTSSLPNVPIRFTKIFVNOQNHVDSGTGKFGHCNIPGLYFAVHITVYMKDVYVS 167
QY 61 LFKDKAMLFYTDYOENNVDSAGSVLLHLEVGQVWLQVYVGGERGLYADNDNSTF 120
DB 168 LYRNKKPVMTFTDQFOSNNVDQAGSVLLHLEVGQVWLQVYVSGSGIYGMINDSTF 227
QY 121 TGFLLYHD 128
DB 228 TGFLLYHD 235
RESULT 14
06GLS9
ID 06GLS9 PRELIMINARY; PRT; 235 AA.
AC 06GLS9;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE MGC84292 protein.
GN Name=MGC84292;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shennen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gamaralle P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzyniński M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Klein S., Gerhard D.S.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC074375; AAH74375.1; -.

DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0006817; P:phosphate transport; IEA.
DR InterPro; IPR001073; Clq.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR008983; TNF_like.
DR Pfam; PF00386; Clq; 1.
DR Pfam; PF01391; Collagen; 1.
DR PRINTS; PR00007; COMPLEMENTC1Q.
DR SMART; SM00110; C1Q; 1.
DR PROSITE; PS01113; C1Q; 1.
KW Collagen.
SQ SEQUENCE 235 AA; 25708 MW; 7B5E24A4BEDBD98 CRC64;

Query Match 67.5%; Score 478; DB 2; Length 235;
Best Local Similarity 65.6%; Pred. No. 3,1e-39; Indels 0; Gaps 0;
Matches 84; Conservative 22; Mismatches 22; Indels 0; Gaps 0;

QY 1 FSVGLETVYTIIPMPIRFTKIFYNQONHYDSTGKPHCNIPGLYFAYHITVYMKDVKVS 60
DB 108 FSMGLSTKPSLPVPIRFTVFNQHRHYDSTGKPSALIKGLYQPSYHLTVYMKDVKVG 167
QY 61 LFKKDKAVLFTYDQYQDNNVDQASGVLLHLEVGDQVYLQVYGBGERNGLYADNDSTF 120
DB 168 LYNNKPRIMFTFDQFSNNVDQASGVLLQLLEVGDIEIWLQYGDSPFSGIYGDNLNDSTF 227
QY 121 TGEIHYD 128
DB 228 SGILLYPD 235

RESULT 15

OGJRSS
ID OGJRSS PRELIMINARY; PRT; 153 AA.
AC OGJRSS;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Adiponectin (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxId=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang G.D.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY320353; AA083880.1; -
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0006817; P:phosphate transport; IEA.
DR InterPro; IPR001073; Clq.
DR InterPro; IPR008160; Clq_helix.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR008983; TNF_like.
DR Pfam; PF00386; Clq; 1.
DR PRINTS; PR00007; COMPLEMENTC1Q.
DR Prodom; PD000007; Clq_helix; 1.
DR SMART; SM00110; C1Q; 1.
DR PROSITE; PS01113; C1Q; 1.
KW Collagen.
FT NON_TER 153
FT NON_TER 153
SQ SEQUENCE 153 AA; 16776 MW; C31F50C9149510EE CRC64;

Query Match 65.5%; Score 464; DB 2; Length 153;
Best Local Similarity 88.4%; Pred. No. 4.8e-38; Indels 0; Gaps 0;
Matches 84; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 1 FSVGLETVYTIIPMPIRFTKIFYNQONHYDSTGKPHCNIPGLYFAYHITVYMKDVKVS 60
DB 59 FSVGLETVYTIIPMPIRFTKIFYNQONHYDSTGKPHCNIPGLYFAYHITVYMKDVKVS 118
QY 61 LFKKDKAVLFTYDQYQDNNVDQASGVLLHLEVGD 95

Db 119 LYKKDKAVLFTYDQYQDKNVDQASGVLLHLEVGD 153

Search completed: May 6, 2005, 17:28:49
Job time : 50.9028 secs

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